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[illegible]

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QY	1200	cgaagccagctcgggcccgggtcgcgcgagctcaagcagttcttcgcgcttgatcaaga	1259
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QY	1260	gcacgcctactgtcgcgaacctgatttcgcgcctgtacgcacagtgcggtcttgatgca	1319
Db	1261	GCACGCACTACTGCTCGAAGCTTGTTCGGCGCTGTGACACAGTGGCGGTGGATGCA	1320
QY	1320	gaagtcacacagaaccggaaccaggt	1346
Db	1321	GAACTCACACAGACCCGAAACCAAGGT	1347

RESULT	4
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LOCUS	AF059293 1716 bp mRNA PRI 02-AUG-1998
DEFINITION	Homo sapiens cytokine-like factor-1 precursor (CLF-1) mRNA,
ACCESSION	AF059293 complete cds.
NID	AF059293
VERSION	93372626
KEYWORDS	AF059293.1 GI:3372626
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS	Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 1716)
JOURNAL	Elson,G.C.A., Graber,P., Losberger,P., Herren,S., Gretenep,D.,
REFERENCE	Memoud,L.N., Wells,T.N.C., Kosco-Vilbois,M.H. and Gauchat,J.F.
AUTHORS	CLF-1, a Novel Soluble Protein Shares Homology With Members of the
TITLE	Cytokine Type-I Receptor Family
JOURNAL	J. Immunol. (1998) In press
REFERENCE	2 (bases 1 to 1716)
AUTHORS	Elson,G.C.A., Graber,P., Losberger,P., Herren,S., Gretenep,D.,
TITLE	Memoud,L.N., Wells,T.N.C., Kosco-Vilbois,M.H. and Gauchat,J.F.
JOURNAL	Direct Submission
REFERENCE	Submitted (14-Apr-1998) Dept. of Immunology, Sero-pharmaceutical
AUTHORS	Research Institute, 14, Chemin des Aulx, Plan-Ies-Ouates, GE 1228,
TITLE	Switzerland
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Query Match 59.4%; Score 967.4; DB 11; Length 1716;
Best Local Similarity 84.1%; Pred. No. 4,56-197;
Matches 118; Conservative 0; Mismatches 201; Indels 10; Gaps 2;

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DB 188 --CTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 244
QY 259 atcagcccccagagcccccacccctctctctctctctctctctctctctctctctctata 318
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QY 319 catgagacacacactgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 378
DB 305 CACGGAGACCCACAGAGGACCCCGCGGCGCTCTACTGAGACCTCAAGGGGCGCGC 364
QY 379 ctgcctctgagctgtctgcgcctctctctctctctctctctctctctctctctctct 438
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QY 499 attctgtctgtctgtctgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 558
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DB 965 GACTGGAAGTGTGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1024
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QY 1099 aagcgagagatctgagagagatgagatgagatgagatgagatgagatgagatgagatgag 1158
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QY 1339 aaccagctc 1347
DB 1325 AACCAAGAC 1333

RESULT 5
LOCUS A70388 834 bp DNA PAT 07-MAY-1999
DEFINITION Sequence 18 from Patent WO9811225.
ACCESSION A70388
NID 94774667
VERSION A70388.1 GI:4774667
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 834)
AUTHORS Nicola, N.A., Farley, A., Nash, A., Willson, T., Rakar, S., Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and Kikuchi, Y.
TITLE A NOVEL HAEMOPHILIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
JOURNAL Patent: WO 9811225-A 19-MAY-1998;
FEATURES
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CDS
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BASE COUNT 167 a 274 c 225 g 168 t
ORIGIN

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Db	661	CGCCTGGCCGGCGTGAACCCGGGACCGGTATCTTACTTGTGTCAAGTGGCGTGCMAACCCCTTT		720
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Db	721	GGCATCTATGGCTCTCAAGAAAGCCGGGATCTGTAGTGTAGTGAGGCAACCCACAGCGCC		780
Qy	1141	TCGACCCCTCGAAGTGAAGCGCCCGGAGCCCGGCGCGGCGTGTGCGAGCCGCGGAGCGC		1200
Db	781	TCGACTCTCCCGCAGTGAAGCCGCCCGGCGCGGCGGCGTGTGCGAAACCGGCGGCGCGA		840
Qy	1201	GAGCGGAGCGCGGAGCGGCGGT		1260
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Qy	1261	CAGCGCAACTGTCTCGGAACCTTAGTTCCTCGGCTGTGAAGCAAGTGTGTGTGTGTGTGTGT		1320
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Qy	1321	AAGTCAACAAGACCCGAAACCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT		1380
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	RESULT	7	A70393	LOCUS	680 bp	DNA	PAT	07-MAY-1999
	DEFINITION	Sequence 23 from Patent WO9811225.						
	ACCESSION	A70393						
	NID	94774671						
	VERSION	A70393.1						
	KEYWORDS	GI:4774671						
	SOURCE							
	ORGANISM	unidentified.						
		unclassified.						
	REFERENCE	Unclassified.						
	AUTHORS	1 (bases 1 to 560)						
		Nicola,N.A., Fabril,L., Farley,A., Nash,A., Willson,T., Rakar,S., Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and Khushf,Y.						
	TITLE	A NOVEL HEMOPOLYMER RECEPTOR AND GENETIC SEQUENCES ENCODING SAME						
	JOURNAL	Patent: WO 9811225 A 19-MAR-1998;						
		NICOA NICOS ANTONIO (AU)						
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	Best Local Similarity	88.0% ; Pred. No. 6,5e+85;						
	Matches	493; Conservative 0; Mismatches 67; Indels 0; Gaps						
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Bd	1	TCGAGCGCAGGGGTGGGGGCACAACCTTGTTGCCACCCGCCGTGACGCACCATCTGGACTT	60					
Oy	508	ggccccccccttatgttttgctctggcccccctgaaagagacccttaaacatcacctctgttc	567					
Bd	61	GCGCCCTGCCCCTATTGTTGGCCTCCCCCAAGAAACCCTCAACATCACCTCTGGTCC	120					
Oy	568	cyygaataagagattcataactcgtgcgcgtcttgacaacctgggttacacyggagagatatcta	627					
Bd	121	AGAACAATGAAGGACCTTAGCTGCCCTGGACGCCACGGCGCCACGCGGAGAGACTTTCCTC	180					
Oy	628	cataccaactactccctcaaagttaaactcgtgatgtagtcaaggtcaagataacatatgtgag	687					
Bd	181	CACACCAACTACTCTCCAAGTACAACCTTAAGGTATGGGTATGCCCAAGAACACATATGTGA	240					

Oy	688	gagtaacacactgtgtgggcccctacatgatgcataatccccaagagccctggccccttact	747
Db	241	GAGTCCACCAAGATGGGGCCCACTCTCGCCACATCCCAAGAGCCCTGGCTCTTTACG	300
Oy	748	ccctatgagatctgtgttgaagaccacacatctgcctatgctcagaacatctgattcttc	807
Db	301	CCCTATGAGATCTGGGTGGAGGACCAACACCGCCTGGGCTCTGCGCCTCGATGTACTC	360
Oy	808	acaatgagatgtctctggacgtgttgaccaagagacccccacccagacgtgtcagttagccgc	867
Db	361	ACGCTGGATATCTCTGGATGTGTGTGACCAACGAGACCCCGCCGACGTGACGTGAGCGCG	420
Oy	868	gttgggggcccggggagaccagctgaagtgtgtgcgtggtgtctcacacacagctctcaagat	927
Db	421	GTCGGGGGCTGGAGAGACCACTTAGGGGTGGCGGTGTGTGCGCACCGCCCTCAAGAT	480
Oy	928	tctccctctccaaagcaagatcacagatcgcctacccgctgtggaagaaacagcgtgactgaag	987
Db	481	TTCCTTTTCAAGCCAATACCAATCCGCTACCGAGTGAAGGACAGTGTGGAATGGAAG	540
Oy	988	gttgttgatgacgttcagcaa	1007
Db	541	GTGGTGAGCAGATGTGACGA	560

RESULT	8			
LOCUS	A70386	938 bp	DNA	PAT 07-MAY-1999
DEFINITION	Sequence 16 from Patent WO9811225.			
ACCESSION	A70386			
MID	94774665			
VERSION	A70386.1	GI:4774665		
KEYWORDS				
SOURCE	unidentified.			
ORGANISM	unidentified			
REFERENCE	unclassified.			
AUTHORS	1 (bases 1 to 938)			
	Nicola,N.A., Fahl,L., Farley,A., Nash,A., Willison,T., Rakar,S., Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and Kikuchi,Y.			
TITLE	A NOVEL HAMPOLEPTIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME			
JOURNAL	Patent: WO 9811225-A 19-MAR-1998;			
	NICOLA NICOS ANTONY (AU)			
FEATURES	Location/Qualifiers			
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ORIGIN				
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Best local Similarity	100.0%;	Pred. No. 3.8e-54;		
Matches 305;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db 1	GGGACCGCTTACTTCGTCCCAAGTCGGTGTAACCATTCGGAGATCTATGGGTGGAANAAG	60		
Oy 1102	ggcggaatctcgagacgaagtcgagaccccccaacgcctgctccaccacctgaatgtagcc	1161		
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QY	1162	ccggagccccgagcgagcgtgtctgcagacgcgggggagcgagcccagaagtccggccgggtg	1221
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QY	1222	cggcgagcgtcaaacgaacttcctccgctcgtcgtcgtcacaagaacgcatactgtctgaacctt	1281
Db	181	C GGCGCGAGCTCAAGCACTTCTCGGCTTGCGCTCAAGAAGACAGCATATGCTCGAACTT	240
QY	1282	agttccgctgtcacgacaaatgaggcgtcttgatgatcagaagtcaacaaaccgaaac	1341
Db	241	AGTTTCGCCCTGTAGACAGCACTGGCGTCTTGATGATGACAAGTAGCACACAAGACCCGAAC	300
QY	1342	caggt 1346 	
Db	301	CAGGT 305	
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LOCUS	A70398	6663 bp	DNA
DEFINITION	Sequence 28 from Patent WO9811225.	PAT	07-MAY-1999
ACCESSION	A70398		
NID	94774676		
VERSION	A70398.1	GI:4774676	
KEYWORDS			
SOURCE	unidentified.		
ORGANISM	unidentified		
REFERENCE	1 (bases 1 to 6663)		
AUTHORS	Nicola,N.A., Fabril,L., Farley,A., Nash,A., Willson,T., Rakar,S., Zheng,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and Kituchi,Y.		
TITLE	A NOVEL HAEMOPHILIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME		
JOURNAL	Patent: WO 9811225-A 19-MAR-1998;		
FEATURES	NICOLA NICOS ANTONY (AU) Location/Qualifiers		
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QY	248	acacagctgtaatcacgccccagagacccacccttcatcgtctcctccctgcaagcta	307
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QY	308	cctgtctatacatgtagagacacaccttggggccaacgcgtgtagggctctactggaacctta	367
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QY	368	atgtgtcgcgcgcgcgcctctgagctgttcccgccctcttaaacacctcaacctgtggccctg	427
Db	1279	ATGATCGCGCCCTGCCCTCTGAGACTGTCCGCTCTCTTAACACTCACCCTTG6CCCTG6	1338
QY	428	cccttgctaaccttaattggttccagagcagaagtcagaagagagaacaattgtytgtcacggc	487
Db	1339	CCCTGGCTATACCTTAATGGGTCCAGGAGAGACAGAGACAMATCGTGTGTGCACGCC	1398
QY	488	gagaagcgagcatctgtgctggtctcctgctctatgttggct 529	
Db	1399	GAGACGCGACACTTGTGCTGCTCCGCTCCGCTATATGTGGCT 1440	
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LOCUS	A70408	11832 bp	DNA
DEFINITION	Sequence 38 from Patent WO9811225.	PAT	07-MAY-1999

ACCESSION	A70408
NID	94774683
VERSION	A70408.1
KEYWORDS	GI:4774683
SOURCE	unidentified.
ORGANISM	unidentified
REFERENCE	unclassified.
AUTHORS	1 (bases 1 to 11832)
TITLE	Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S., Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and Kikuchi,Y.
JOURNAL	A NOVEL HAEMOPHEIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
FEATURES	Patent: WO 9811225-A 19-MAR-1998;
source	NICOIA NICOS ANTONY (AU)
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Best Local Similarity	99.6%; Pred. No. 4.9e+49;
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Dn	6510 CCCTGGCTAACCTTAATGTGGTCCAGCGACAGTCAAGAGACAATCTGGTGTGCACGCC 6569
Dn	488 gagacgagcagcattctgctgtgcctccgcctctatgtttgact 529
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RESULT 11	
LOCUS	AC003112/c 40668 bp DNA PRI 21-NOV-1997
DEFINITION	Human DNA from chromosome 19 specific cosmid R30292, genomic
ACCESION	AC003112 sequence, complete sequence.
NID	92636669
VERSION	AC003112.1 GI:2636669
KEYWORDS	HTG.
ORGANISM	human.
SOURCE	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS	Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE	1 (bases 1 to 40668)
JOURNAL	Lamerdin,J.E., McCreedy,P.M., Adamson,A.W., Burkhardt-Schultz,K., Gordon,L., Christensen,M., Kyle,A., Ramirez,M., Stillwagen,S., Gaines,J., Dangnan,L., Bruce,R., Quan,G., Montgomery,M., Ow,D., Kobayashi,A., Olsen,A.O. and Carraro,A.V.
	Sequence analysis of an ~1 Mb region containing the MEF2B gene in
	19912
	Unpublished
	2 (bases 1 to 40668)
	Lamerdin,J.E.
	Direct Submission
	Submitted (21-NOV-1997) Human Genome Center, Lawrence Livermore
	National Laboratory, 7000 East Ave., Livermore, CA 94551, USA

FEATURES

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repeat_region
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NBHn19W Homo sapiens cDNA clone 365523 3' (429..307): 95%
identity.----(1127..11246) DDS similarity to AA047548
zf15e02.r1 Soares fetal heart NBHh19W Homo sapiens cDNA
clone 377018 5' (222..341): 97% identity.---(11051..11331)
Predicted exon, program: grall2exons_human_1.3, frame: 0,
quality: good, score: 73.000--(11061..11209) DDS
similarity to AA452628 zc33f04.r1 Soares total fetus
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to AA009693 zeb2h02.s1 Soares fetal heart NBHn19W Homo
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identity.---DDS similarity to AA450010 zc33f04.s1 Soares
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clone 365523 5' (428..496): 97% identity.---(13756..13984)
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NBHn19W Homo sapiens cDNA clone 365523 3' (227..1): 98%
identity.---(13756..13984) DDS similarity to AA450010
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to W71715 zb2h02.r1 Soares fetal lung NBHh19W Homo
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clone 490004 3' (342..1): 99% identity.---(15227..14885)
DDS similarity to AA127694 zK89c11.r1 Soares pregnant
uterus NBHPU Homo sapiens cDNA clone 490004 5' (126..467): 99%
identity.---(15227..14897) DDS similarity to W46603
zc32h10.r1 Soares senescent fibroblasts NBHSF Homo sapiens
cDNA clone 324067 5' (328..1): 99%
identity.---(15227..15088) DDS similarity to W46604
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cDNA clone 324067 3' (332..465): 96% identity.---
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pregnant uterus NBHPU Homo sapiens cDNA clone 490004 3'
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zK89e11.r1 Soares pregnant uterus NBHPU Homo sapiens cDNA
clone 490004 5' (77..125): 90% identity.---(15735..15713)
DDS similarity to W46603 zc32h10.r1 Soares senescent
fibroblasts NBHSF Homo sapiens cDNA clone 324067 5'
(351..329): 100% identity.---(15735..15713) DDS similarity
to W46604 zc32h10.s1 Soares senescent fibroblasts NBHSF
Homo sapiens cDNA clone 324067 3' (299..321): 100%
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[illegible]

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[illegible]

Search completed: September 28, 1999, 16:36:58
Job time: 6805 sec

Query Match	3.3%	Score 53.2;	DB 17;	Length 6633;
Best Local Similarity	59.1%;	Pred. No. 0.1;		
Matches	91;	Conservative	0;	Mismatches 63;
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			Gaps	0

[illegible]

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Db     1051  CGAGGGAGCTGTGGATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY  1111
QY      93  tctcagtcacgcgcgcctctgcgcgcaccccaatgcccgcgggtcgcgccgcgcgcctgc  152
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: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible

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GenCore version 4.5
Copyright (c) 1993 - 1998, Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 28, 1999, 14:43:35 ; Search time 303.81 Seconds

(without alignments)
1341.506 Million cell updates/sec

Title: US-09-037-657-12

Perfect score: 1629

Sequence: 1 ggcacgagcttcgtctccg.....aaaaaaaaaaaaaaaa 1629

Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database: N_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1629	100.0	1629	1	V27140	Novel haemopoietin
2	1563.4	96.0	1673	1	V27141	Novel haemopoietin
3	1532.8	94.1	1656	1	V41688	Nucleotide sequence
4	1339.2	82.2	1724	1	V70896	CDNA encoding rat
5	1335	82.0	1930	1	V27158	Unspliced murine N
6	966.6	59.3	1690	1	V70894	CDNA encoding huma
7	961.4	59.0	1813	1	V70895	CDNA encoding an a
8	932.4	57.2	1579	1	V41689	Nucleotide sequenc
9	830.8	51.0	834	1	V27143	Nucleotide sequenc
10	799.4	49.1	1391	1	V27144	PCR product for hu
11	452.8	27.8	560	1	V27159	Novel haemopoietin
12	305	18.7	938	1	V27142	Nucleotide sequenc
13	280.4	17.2	11832	1	V27148	Nucleotide sequenc
14	280.4	17.2	6663	1	V27145	Nucleotide sequenc
15	178.8	11.0	259	1	V70897	Expressed sequence
16	120.2	7.4	210	1	V70899	Expressed sequence
17	53.2	3.3	12001	1	V76213	HSV L/ST region. H
18	53.2	3.3	4257	1	V10362	Infected cell prot
19	53.2	3.3	4257	1	V68520	The nucleotide seq
20	51.6	3.2	114955	1	X53491	Human adenovine Al
21	51.2	3.1	12827	1	V09036	Equine arteritis v
22	51.2	3.1	15528	1	V09039	Equine arteritis v
23	49.8	3.1	1610	1	O57657	Allele D4.7 of the
24	49.8	3.1	1608	1	T27547	Recombinant human
25	49.2	3.0	345	1	T40297	Human dopamine D4
26	48.6	3.0	985	1	N90929	Non-overlapping re
27	47.2	2.9	1934	1	T13229	OR-1 orphan recept
28	46.8	2.9	1111	1	V43617	Polydeoxyribonucle
29	46.2	2.8	1134	1	V61334	Human secreted pro
30	46.2	2.8	1134	1	V61335	Batten disease gen
31	46.2	2.8	1132	1	T61336	Batten disease gen
32	46.2	2.8	1132	1	T61337	Batten disease gen
33	46.2	2.8	1132	1	T61338	Batten disease gen
34	46.2	2.8	1132	1	T61339	Batten disease gen
35	46.2	2.8	1133	1	T61340	Batten disease gen
36	46.2	2.8	1133	1	T61341	Batten disease gen
37	46.2	2.8	1133	1	T61342	Batten disease gen
38	46.2	2.8	1133	1	T61343	Batten disease gen
39	46.2	2.8	1133	1	T61344	Batten disease gen
40	46.2	2.8	1133	1	T61345	Batten disease gen
41	46.2	2.8	1133	1	T61346	Batten disease gen
42	46.2	2.8	1133	1	T61347	Batten disease gen
43	46.2	2.8	1133	1	T61348	Batten disease gen

ALIGNMENTS

RESULT	ID	Query Match	Score	DB	Length	Matches	Mismatches	Indels	Gaps
1	V27140	100.0%;	1629;	1;	1629;	1629	0;	0;	0;
AC	V27140	Best Local Similarity	100.0%;	Pred. No. 0;					
AC	V27140	Matches 1629;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps
AC	V27140	Standard; CDNA; 1629 BP.							
DE	29-SEP-1998 (first entry)								
DE	Novel haemopoietin receptor NR6.1 gene.								
KW	Haemopoietin receptor; cell proliferation; cell differentiation; cancer;								
KW	cell survival; therapeutic; neuronal proliferation; drug screening; ss;								
OS	Mouse.								
OS	Mus sp.								
FT	Key	Location/Qualifiers							
FT	CDS	113..1355							
FT		/tag= a							
FT		/product= "Haemopoietin receptor NR6.1"							
PN	W09811225-A2.								
PD	19-MAR-1998.								
PF	11-SEP-1997; G02479.								
PR	11-SEP-1996; AU-002246.								
PA	(AMRA-) AMRAD OPERATIONS PTY LTD.								
PI	(DZIE/) DZIELEWSKA H E.								
PI	Alexander W, Fabril L, Farley A, Hilton DJ, Kikuchi Y,								
PI	Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willison T,								
PI	Zhang J;								
DR	WPI: 98-260970/23.								
DR	P-PSDB; W55011.								
PT	New isolated haemopoietin receptor - used for developing products								
PT	for modulating proliferation, differentiation and survival of cells,								
PT	e.g. neuronal cells								
PS	Claim 4: Page 77-81; 182pp; English.								
CC	The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6.								
CC	interaction between the novel HR and a ligand facilitates proliferation,								
CC	differentiation and survival of a wide variety of cells. The HR and its								
CC	derivatives can be used for modulating the activity of the receptors e.g.								
CC	to regulate development, maintenance or regeneration in an array of								
CC	different cells and tissues in vitro and in vivo. They can be present in								
CC	therapeutics used for modulating neuronal proliferation, differentiation								
CC	and survival. The products can also be used for detection and diagnosis,								
CC	e.g. for cancers or predisposition to cancers, or for drug screening.								
CC	Sequence 1629 BP; 336 A; 541 C; 453 G; 299 T;								
QQ									
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Db	361	ACCCTGAATGATGCGCGCTGCCCTCTGTAGCTGTCCCGCTCTTAACACTCCACCGCTG	420
Qy	421	gcccttgcccttgcttaacttaatggtctccagcgacgaatgaagacatctgtygt	480
Db	421	GCCCTGGCCCTGGCTTAACCTTAATGGGTCCAGCGACGAGTAAAGAGCAACTGTGTGT	480
Qy	481	cagcgccgaagcagcgacatctctgctgctcctcctatgtytgctgccccctgag	540
Db	481	CAGCGCCGAGAGCGGACGATCTTGCTGGCTCTCTCTATGTTGGCTGCCCTCGAG	540
Qy	541	aagcccttaaacatcagctcgtctgctccgcgaaatgaaagatctccacgtgcgctgaca	600
Db	541	AAGCCCTTAACATCAGCTGCTGTGTCGCCGAACATGAAGATATCAGCTGCCGTGACA	600
Qy	601	cgcggtgcacacgvggagacatctcttaataaccaactctccccaagtacaagctgag	660
Db	601	CGCGGTGCACACGGGAGACATTTCTTAATACCAACTCTCCCTCAATCAACCTGAGG	660
Qy	661	tgtctacgtaagataaacatctgttagagagtaaccaactcgtgggcccctcatatgcat	720
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Qy	721	atccccaagaagccttgccctctctcaactccctatgagatctggttgaaagccacaatcgc	780
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Qy	781	ctagagctcagcaaatctatctctcaacatcgtatctccctgagacgtgtgtaccaagagc	840
Db	781	CTAGAGCTCAACAAGATCTATGTCTTCACACTGAGATGTCTGTGATGTATCCACCGAC	840
Qy	841	ccccccaccgacagctgacgttgagccgcgcttgaggccctggagagaccacgtagctgtgc	900
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Qy	901	tgaggtctcaaccacagctctcaagagatcttcctcttccaaagccaagtacaagatccgtac	960
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Db	1321	AAGTCACACAAGACCGCAAAACAGGTCCTCCGGCTAAACTGTAAGGATAGGCCATCTCTC	1380
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Db	1261	GCACGCATACGTGCTGSAAGCTTAGTTCCGCCCTGTACGACAGTGGCTTGATGCA	1320
OY	1320	gaagtcacacaagaccgaaac-----	1343
Db	1321	GAATCACAACAAGCCCCGANAACAGACGAGGGGATCCTGCCTTGGGGCAGAGGGGCTGC	1380
OY	1343	-----agcttcgcgcgtctaaaccttaagatagcatalcctcctgtctggtcagacct	1396
Db	1381	GGCGAGAGGCTCTGCGGGTTAACTCTAAGAGATAGGCCATCCTCTGCTGGGTACGACT	1440
OY	1397	ggagagctcaccttaattgagagccctctgtaccatctgggcacaagaacactacaga	1456
Db	1441	GGAAGCTCACCTAAATTGGAGCCCCCTGTACCATCTGGGCAACAAGAACTACACGA	1500
OY	1457	ggctcggggcacaaatgagctccccaacacacacagcttgytccaatgatgtcacacttg	1516
Db	1501	GGCTGGGGCAATGAGCTCCCAACAACACACTTGTGGTCCACATGAGTGCACACTTGG	1560
OY	1517	ataaccccaagtgtggtgaagtgtgggattgagggcctccccaacatctcttaaat	1576
Db	1561	ATATACCCCATGTGTGGTAAAGTGTGGGGATTGCGAGGCGCTCCCAACATCTCTTAAAT	1620
OY	1577	aaataaaggagttctcaggtaaaaaanaaaaaaanaaaaaaanaaaaaa 1629	
Db	1621	AAATTAAGAGGCTGTTCAAGTAAATAAATAAATAAATAAATAAATAAATAA 1673	

Query Match	94.1%	Score 1532.8;	DB 1;	Length 1656
Best Local Similarity	96.7%	Pred. No. 0;		

[illegible]

QY	1085	tccttggtctgaaaaagggcggaatcttgagagagatggagacacccacccgcctgcctcca	1144
Db	1083	TCATGGGCTGAAAAAGGGCGGGANATTGGAGCGAGCTGGAGCCACCCTCCTCTCA	1142
QY	1145	ccccctcgaagtgaagccgcccgagcccgagcgaggggtgtgtgcagagccgagggcgagc	1204
Db	1143	CCCCTCGAAGTGAAGCGCGCGCGGCCCGGGGGGGGTGTCGAGCCGCGGGGCGAGNC	1202
QY	1205	ccagctcgggcccgggtgctgagcgagcttaagcaagttctctggctcggtctcaagaagcag	1264
Db	1203	CCACACTGGGGCCGGGTGCGCGCGGACCTCAACAGATCTCTGCGGTCAAGAGCAGC	1262
QY	1265	catatctctcgaaccttaagttcttcgcgcgttaagaccaagtgagcttgagatgcagaagt	1324
Db	1263	CATATCTCTCGAAGCTTAAGTTTCCGCTGTACGACCAAGTGGCTCTTGATGCAGAACT	1322
QY	1325	cacacaaagcccgaaacc-----	1343
Db	1323	CACACAAAGACCCGAAACCAAGAGGAGGATCCCTCGGCGGACAGGGGGTGGCGGA	1382
QY	1343	-aggtcttgccggcttaaaccttaagatagagcgaatcctctctgtgtcgaagcctgagag	1401
Db	1393	GAGGTCTCTGCGCGGTAAACTCTAAGGATAGGGCATCTCTCTGTGGTGAAGCTGGAGG	1442
QY	1402	ctcacctgaaatgagacccctctgtacacatctggcgcaacaagaacctacagagagctg	1461
Db	1443	CTCACCTGAANTGAGAGCCCTCTGTACATCTGTGGCAAAAGAAACCTACAGAGGCTG	1502
QY	1462	gggcacaatgagctcccaacaacacacagcttgggtccacatgagtgatcaacttgatata	1521
Db	1503	GGGCACATGAGCTCCACACACACAGCTTTGGTCCACATGATGGTTCACACTTGGATATA	1562
QY	1522	ccccagtggtgagaaagttgggtatttgaaagggccctcccaaatctcttaaaaaata	1581
Db	1563	CCCCAGTGTGGGTAGGGTTGGGTATTTGACGGGGCTCCCAAGATCTCTTTAAATATAA	1622
QY	1582	aaggagttgttcaggtataaaaaaaa 1609	
Db	1623	AAGGAGTTGTTCACGCTCCGAAAAAAA 1650	
RESULT 4			
QY	V70896		
ID	V70896 standard; cDNA; 1724 BP.		
AC	V70896:		
DT	17-MAR-1999. (first entry)		
DE	cDNA encoding rat Zcyto5.		
KW	Zcyto5; cytokinin-like receptor; down-regulation; growth factor;		
KW	maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;		
KW	cardiac pathology; heart enlargement; Zcyto5 ligand; ss.		
OS	Rattus sp.		
PH	Key	Location/Qualifiers	
FT	CDS	159..1436	
FT		/*tag= a	
FT		/product= zcyto5	
PN	W09849307-A1.		
PD	05-NOV-1998.		
PF	01-MAY-1998; U08865.		
PR	13-FEB-1998; US-074721.		
PR	01-MAY-1997; US-045287.		
PR	01-MAY-1997; US-850030.		
PR	13-FEB-1998; US-023890.		
PI	(Zymo) ZYMOGENETICS INC.		
PI	Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,		
PI	Lok S, Presnell SR, Whitmore TE;		
DR	WPI: 99-034662/03.		
DR	P-ESDB: W70862.		
PT	New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.		
PT	down-regulating Zcyto5 natural ligands or detecting cardiostrophin-1		
PS	in blood		
PS	Disclosure: Page 72-75; 55pp. English.		
CC	The present sequence encodes a protein designated zcyto5, which is		

PS Disclosure: Page 63-66; 55pp; English.
 CC The present sequence encodes a protein designated Zcytors, which is
 CC a cytokinin-like receptor. Soluble Zcytors may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytors could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible Zcytors ligands. A probe
 CC comprising Zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytors gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytors and
 CC therapeutically to modify Zcytors ligand effects.
 SO Sequence 1650 BP; 319 A; 592 C; 505 G; 274 T;

Query Match 59.3%; Score 966.6; DB 1; Length 1690;
 Best Local Similarity 85.6%; Pred. No. 1.5e-191;
 Matches 1090; Conservative 0; Mismatches 174; Indels 9; Gaps 1;

75 cccgcgccatcacgcggtgtgacgtacccggtgtgctgcgcaccccatgcccgcgag 134
 3 CCACGCGCGGAGCCG 62
 135 tggccgcgccccggtgtgccccatccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 194
 63 CCGCGGGGGCCCCCGCCCAATCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 121
 195 gtcgcctcgt 254
 121 -----CTGCTGCTGTGCTCTCTCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 173
 255 tgaatcacccccagagaccctctctatcgcgtcctcctcgaagctcgcgcgcgc 314
 174 TGTGATCACTCCCGAGATCCAGAGCTTCTCATCGGCTCTCTCTGCGCCAGCTGCTC 233
 315 tttatcgtgagacacacccgtgggcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 374
 234 AGTGCAGGAGAGCCACCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 293
 375 cgcgcgtcctcgtgagctcctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 434
 294 CCGCTGCG 353
 435 taacttaagtggtccagc 494
 354 CAACCTCATATGCTCCAGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 413
 495 cagcattctgtgctcctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 554
 414 CAGCATCTCTGCTGCT 473
 555 cagcgtcgt 614
 474 CAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 533
 615 ggaagacattctacatacctacccctcaagatacagcgcgcgcgcgcgcgcgcgcgc 674
 534 GGAAGACTTCTCCACACCACTACTCTCTCAAGTACAGCTTGTGTGTGTGTGTGTGT 593
 675 taacacatgtgaggtacacacacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 734
 594 CAACACATGTGAGGTACACACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 653
 735 ggcctcttcatcctcatgagatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 794
 654 GGCCTCTTTTACGCTTACAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 713
 795 acatgtatcctcacactgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 854
 714 CTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 773
 855 gcaagtgtgacgcgt 914

DB 774 GCACGTGAGCCCGCTGCGGGGCGCTGTGAGAGACCGAGCTGAGCTGTGCTGCCAC 833
 QY 915 agcttcaagatcttcttccaaagcacaagraccaagatcgcgtcgcgtgtgagacag 974
 DB 834 CCGCTCAAGGATTTCTCTTTCAGCCAAATACAGATCCCTCTCCAGTGTGAGAGAC 893
 QY 975 cgtgactgaaagt 1034
 DB 894 TGTGAGCTGGAAGT 953
 QY 1035 gaagccgcgcacggttacttgcacaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1094
 DB 954 GAACCCGCGACCGTGTACTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1013
 QY 1095 gaaagagcgggaatctgtgagcagatgtgagcaccacacgcgtcctcaccctgaag 1154
 DB 1014 CAGAAAGCCGGGATCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1073
 QY 1155 tgaagc 1214
 DB 1074 TGAAGCCTCCG 1133
 QY 1215 cccggtgc 1274
 DB 1134 GCGGTCG 1193
 QY 1275 gaacttgaattcgcgcgt 1334
 DB 1194 CAACCTCAAGCTTCCCTCTACAGACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1253
 QY 1335 cggaaacaggtgc 1347
 DB 1254 CCGCAACCGAGAC 1266

RESULT 7
 ID V70895 standard; cDNA; 1813 BP.
 AC V70895.
 DT 17-MAR-1999 (first entry)
 DE cDNA encoding an allelic variant of human Zcytors.
 KW Zcytors; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 KW cardiac pathology; heart enlargement; Zcytors ligand; allelic variant;
 KW ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 88..1365
 FT /tag= 8
 FT /product= Zcytors
 FN W09849307-A1.
 PD 05-NOV-1998.
 PR 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 DR P-PSDB: W70861.
 PT New mammalian cytokinin-like receptor Zcytors - useful for, e.g.,
 PT down-regulating Zcytors natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Disclosure: Page 68-70; 55pp; English.
 CC The present sequence encodes an allelic variant of protein designated
 CC Zcytors, which is a cytokinin-like receptor. Soluble Zcytors may be
 CC administered to down-regulate the effects of a growth and/or maintenance
 CC factor in thyroid, heart, and skeletal muscle for example to lessen the
 CC effect of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytors could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible Zcytors ligands. A probe

Db 961 AAGTGCACAGAGCCCGACACAGACAGAGAGC 993

RESULT 11

V27159 standard; DNA: 560 BP.

AC V27159;

DE 29-SEP-1998 (first entry)

KW Haemopoietin receptor; cell proliferation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening; ss;

OS Homo sapiens.

PN M09811225-A2.

PD 19-MAR-1998.

PF 11-SEP-1997; G02479.

PR 11-SEP-1996; AU-002246.

PA (AMRA-) AMRAD OPERATIONS PTY LTD.

PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y, Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T, Zhang J, Zhang J.

PI WPI; 98-260970/23.

DR New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells

PS Disclosure: Page 101, 182pp; English.

CC NR6 is a novel haemopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and its derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

CC Sequence 560 BP; 113 A; 182 C; 165 G; 100 T;

SQ

Query Match 27.8%; Score 452.8; DB 1; Length 560;

Best Local Similarity 88.0%; Pred. No. 2.3e-85;

Matches 493; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 448 tccaggagcagctgaagacacatctgtgtgtcaagccgagagagagacatttgcct 507

Db 1 TCCAGGAGCGCGTGGGGGACACCTCTGTGCGACGCCGCTGAGCGAGATCCTGCT 60

QY 508 ggcctccgctctatgt 567

Db 61 GGCCTCGCTCTATGT 120

QY 568 cggacacatgaagatctcaagctgcgcgtgcacacgggtgcacacggggagacattctta 627

Db 121 AAGAAATGAAGACTTGACTGCGCTGGAGCGCAGGGGCCACAGSGGAGACCTTCTC 180

QY 628 catcaacactctccctcaagtacagctgagtggtgtgtgtgtgtgtgtgtgtgtgtgt 687

Db 181 CACACCACTACTCCCTCAAGTACAGCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240

QY 688 gagacacacactgtggggccctcactcatatccccaaggagctgtgaccttcaact 747

Db 241 GAGTACCAACAGTGGGGCCCACTCTGCGACATCCCAAGGAGACTGTGCTTTTACG 300

QY 748 cccatagatctgt 807

Db 301 CCCATGATGATCTGGGTGGAGGACCAACCGCTGGCTGTGCGCTCCGATGTACTC 360

QY 808 acactgt 867

Db 361 ACCTGTGATATCTGT 420

QY 868 gt 927

Db 421 GTCGGGGGCTTGAGAGACAGCTGAGCTGGGTGTGCGCAACCCGCTCAAGAT 480

QY 928 ttcctctccaaagccaaagttaccagatccgctacacgctggagagacgctgactgag 987

Db 481 TTCCTTTTCAAGCAATACCAATCCGCTACCGAGTGGAGACAGTGTGATGAG 540

QY 988 gt 1007

Db 541 GTGTGTGAGATGTGAGCA 560

RESULT 12

V27142 standard; DNA: 938 BP.

AC V27142;

DE 29-SEP-1998 (first entry)

KW Haemopoietin receptor NR6.3 gene.

KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening; ss;

OS Mouse.

PN Mus sp.

PI Key

FT CDS

FT Location/Qualifiers

FT 1. 468

FT /tag- a

FT /product- "Haemopoietin receptor NR6.3"

FT M09811225-A2.

PD 19-MAR-1998.

PF 11-SEP-1997; G02479.

PR 11-SEP-1996; AU-002246.

PA (AMRA-) AMRAD OPERATIONS PTY LTD.

PI (DIE/) DIEGLEWSKA H E.

PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y, Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T, Zhang J, Zhang J.

PI WPI; 98-260970/23.

DR P-PSDB; W55013.

PT New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells

PS Claim 6: Page 90-92; 182pp; English.

CC The haemopoietin receptor (HR) NR6.3 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and its derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

CC Sequence 938 BP; 243 A; 245 C; 272 G; 178 T;

SQ

Query Match 18.7%; Score 305; DB 1; Length 938;

Best Local Similarity 100.0%; Pred. No. 9.5e-55;

Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1042 ggcacgcttactctgcgcacagtgctgttaacccattggagatctgtgtgtgtgtgtgtgt 1101

Db 1 GGCACCGCTTACTCTGCACAGT 60

QY 1102 cggggaacttgagacgagtgagacacacacacacacacacacacacacacacacacacac 1161

Db 61 GCGGGAATCTGAGACGAGTGGAGACCAACCGCTGCTCCACCTCCAAATGAGAGC 120

QY 1162 cgggcccggggcgggggt 1221

Db 121 CCGGGCCCGGGGGGGGGGT 180

QY 1222 cggcgagagctcaagcgt 1281

Db 181 CGGCGCAGCTCAAGCACTTCTGCTGCTGCTCAAGAGACACCATACTGTAACCTT 240

QY 1382 agttccgctgtacagaccagtggtgctgtgtaagtcagaaatcacacagaccgaac 1341
 DB 241 AGTTCCGCCCTGTACGACACCATGTGCTGTGATGACAGAGTACACAGACCCGAAAC 300
 QY 1342 cagct 1346
 DB 301 CAGCT 305

RESULT 13

V27148
 ID V27148 standard; DNA; 11832 BP.
 AC V27148;
 DT 29-SEP-1998 (first entry)
 DE Nucleotide sequence for murine NR6 containing additional 5N sequence.
 KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
 KM Cell survival; therapeutic; neuronal proliferation; drug screening; ss;
 OS Mus sp.
 PN MO9811225-A2.
 PD 19-MAR-1998.
 PF 11-SEP-1997; G02479.
 PR 11-SEP-1996; AU-002246.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI (DZIE/) DZIEGLEWSKA H E.
 PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willison T,
 PI Zhang J, 98-260970/23.
 DR WPI; 98-260970/23.
 PT New isolated haemopoietin receptor - used for developing products
 for modulating proliferation, differentiation and survival of cells,
 e.g. neuronal cells
 PS Claim 9: Fig 3: 182pp; English.
 CC The NR6 protein is a novel Haemopoietin receptor (HR). Interaction
 CC between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and its
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 11832 BP; 2447 A; 3367 C; 3298 G; 2720 T;

Query Match 17.2%; Score 280.4; DB 1; Length 11832;
 Best Local Similarity 99.6%; Pred. No. 1.9e-49;
 Matches 281; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 248 acacagctgtatcagccccagagaccaccccttcctcagctcctccctcgaagcta 307
 DB 6330 ACACAGCTGTATCAGCCCCAGAGACCCACCTTCATCGGCTCCTCCCTCAAGCTA 6389
 QY 308 cctgctctatcatatgagacacacacctggggccacagctgaggggctactgaacctca 367
 DB 6390 CCTGCTCTATATCATGAGAGACACACACTGGGGCCACCGCTGAGGGCTTATGACCTTCA 6449
 QY 368 atggtgcgcgcctgcccctgagctgtccgcctccttaaacacctccacctggccctg 427
 DB 6450 ATGGTCCGCCGCTGCTGTGAGCTGTCCGCCCTTACACCTCCACCTGAGCCCTG 6509
 QY 428 cccctggttaaccttaaggttccagagcagatcagaggaacatcgtgtgtcaagccc 487
 DB 6510 CCCCTGGCTAATCACTTAATGGGTCCAGGACAGTCAAGAGACAATCGTGTGTACAGCCC 6569
 QY 488 gagagcgagcagatcctgctgctgctcctcctcctatgttgct 529
 DB 6570 GAGAGCGCAGCATTTCTGCTGCTGCTCCTCTATGTTGCT 6611

RESULT 14
 V27145
 ID- V27145 standard; DNA; 6663 BP.

AC V27145;
 DE 02-OCT-1998 (first entry)
 DT Nucleotide sequence of Murine NR6.
 KW Haemopoietin receptor; cell proliferation; cell differentiation;
 KM Cancer; cell survival; therapeutic; neuronal proliferation; drug;
 OS Mus sp.
 PN MO9811225-A2.
 PD 19-MAR-1998.
 PF 11-SEP-1997; G02479.
 PR 11-SEP-1996; AU-002246.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI (DZIE/) DZIEGLEWSKA H E.
 PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willison T,
 PI Zhang J, 98-260970/23.
 DR WPI; 98-260970/23.
 PT New isolated haemopoietin receptor - used for developing products
 for modulating proliferation, differentiation and survival of cells,
 e.g. neuronal cells
 PS Claim 8: Page 108-114; 182pp; English.
 CC The NR6 gene encodes a novel Haemopoietin receptor (HR). Interaction
 CC between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and its
 CC products can be used for modulating the activity of the receptors e.g. to
 CC regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 6663 BP; 1462 A; 1852 C; 1715 G; 1634 T;

Query Match 17.2%; Score 280.4; DB 1; Length 6663;
 Best Local Similarity 99.6%; Pred. No. 1.7e-49;
 Matches 281; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 248 acacagctgtatcagccccagagaccaccccttcctcagctcctccctcgaagcta 307
 DB 1159 ACACAGCTGTATCAGCCCCAGAGACCCACCTTCATCGGCTCCTCCCTCAAGCTA 1218
 QY 308 cctgctctatcatatgagacacacacctggggccacagctgaggggctactgaacctca 367
 DB 1219 CCTGCTCTATATCATGAGAGACACACCTGGGGCCACCGCTGAGGGCTTATGACCTTCA 1278
 QY 368 atggtgcgcgcctgcccctgagctgtccgcctccttaaacacctccacctggccctg 427
 DB 1279 ATGGTCCGCCGCTGCTGTGAGCTGTCCGCCCTTACACCTCCACCTGAGCCCTG 1338
 QY 428 cccctggttaaccttaaggttccagagcagatcagaggaacatcgtgtgtcaagccc 487
 DB 1339 CCTGGCTAATCACTTAATGGGTCCAGGACAGTCAAGAGACAATCGTGTGTACAGCCC 1398
 QY 488 gagagcgagcagatcctgctgctgctcctcctcctatgttgct 529
 DB 1399 GAGAGCGCAGCATTTCTGCTGCTGCTCCTCTATGTTGCT 1440

RESULT 15

V70897
 ID V70897 standard; CDNA; 259 BP.
 AC V70897;
 DT 17-MAR-1999 (first entry)
 DE Expressed sequence tag used to identify human zcytores.
 KW zcytores; cytokinin-like receptor; down-regulation; growth factor;
 KM Maintenance factor; thymoid; heart; skeletal muscle; cardiomyophin-1;
 KM cardiac pathology; heart enlargement; zcytores ligand; EST; ss.

OS Unidentified.
PN WO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998: U08865.
PR 13-FEB-1998: US-074721.
PR 01-MAY-1997: US-045287.
PR 01-MAY-1997: US-850030.
PR 13-FEB-1998: US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE.
DR WPI, 99-034662/03.
PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
PT down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
PI in blood
PS Example 1: Page 77: 55pp: English.
CC The present sequence represents an expressed sequence tag (EST)
CC used to identify cDNA encoding a protein designated Zcytor5, which is
CC a cytokinin-like receptor. Soluble Zcytor5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thymoid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the
CC blood, and to discover other possible Zcytor5 ligands. A probe
CC comprising Zcytor5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcytor5 and
CC therapeutically to modify Zcytor5 ligand effects.
SQ Sequence 259 BP; 53 A; 64 C; 81 G; 46 T;

Query Match 11.0%; Score 178.8; DB 1; Length 259;
Best Local Similarity 81.3%; Pred. No. 9,4e-29;
Matches 209; Conservative 0; Mismatches 47; Indels 1; Gaps 1;
QY 923 aggaattccttccaagcaagtaaccagatccgctacgcgtgagagacgctgact 982
DB 1 AGGATTCTCTTTCAGCAATACCAATACGATCCGCTANCGAGTGGAGAGANAGTGGANT 60
QY 983 ggaagtggtgatgacgtcagaacacacacacacacacacacacacacacacac 1042
DB 61 GGAAGGTGTTGGATGATGAGCAACCAACCAACCAACCAACCAACCAACCAACCAAC 119
QY 1043 gacacgttacttcgacagtgacgtgtgaaccacatcgagatcctatggtgaaag 1102
DB 120 GCANCGTACTTCTGCGCAGTGCCTGCAANCCCTTGGCATCTATGGCTNCAAGAAAG 179
QY 1103 cgggaatctgagcgagtgagagcaccacacacacacacacacacacacacacac 1162
DB 180 CCGGGAJCTNGAGTGTGAGTGAGCCANCCACACAGCCGCTTCANTTCCCGCAGTACG 239
QY 1163 cgggcccgagcgagcg 1179
DB 240 NCGGCCCGGNGNGNGG 256

Search completed: September 28, 1999, 16:44:42
Job time: 7267 sec

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OM nucleic - nucleic search, using SW model

Run on: September 28, 1999, 14:43:32 ; Search time 2095.87 Seconds

(without alignments)
1533.138 Million cell updates/sec

Title: us-09-037-657-12

Perfect score: 1629

Sequence: 1 ggcacgagctcgtcgtcgcg.....aaaaaaaaaaaaaaaaaaaa 1629

Scoring table: IDENTITY_NUC

Searched: 2546578 segs, 98626752 residues

Database :

EST:
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: em_est20:*
21: em_est21:*
22: em_est22:*
23: em_est23:*
24: em_est24:*
25: em_est25:*
26: em_est26:*
27: em_est27:*
28: em_est28:*
29: em_est29:*
30: em_est30:*
31: em_est31:*
32: em_est32:*
33: em_est33:*
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37: em_est37:*
38: em_est38:*
39: em_est39:*
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41: em_est41:*
42: em_est42:*
43: em_est43:*
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46: em_est46:*
47: em_est47:*
48: em_est48:*
49: em_est49:*
50: em_est50:*
51: em_est51:*
52: em_est52:*
53: em_est53:*

54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	464	28.5	464	29	AA049280
2	457.8	28.1	482	26	W66776
3	391.8	24.1	428	45	AA866388
4	364.2	22.4	474	46	AI421423
5	362.8	22.3	477	43	AI185924
6	356.6	21.9	503	29	AA049278
7	355.4	21.8	462	45	AI394468
8	354	21.7	466	43	AI161002
9	354	21.7	466	43	AI185780
10	337.8	20.7	445	27	AA039053
11	334	20.5	447	45	AI187074
12	324.2	19.9	431	45	AI333812
13	311.4	19.1	417	44	AI269388
14	296.8	18.2	332	48	AI579568
15	284.4	17.5	319	48	AI574687
16	284.2	17.4	385	50	AI570108
17	283.6	16.2	390	26	W17583
18	266.4	15.1	410	27	AA042914
19	230.6	14.2	470	43	AI233311
20	226	13.9	464	41	AI071408
21	216.2	13.3	262	50	AV032198
22	202	12.4	235	48	AI575060
23	195.2	12.0	458	27	AA043001
24	191.2	11.7	465	26	W46604
25	185.8	11.4	273	23	R87407
26	172	10.6	229	49	AV010798
27	149.4	9.2	167	49	AV011309
28	146.6	9.0	455	46	AA925924
29	131.8	8.1	218	22	H14009
30	129.8	8.0	237	25	N78873
31	118.4	7.3	227	30	AA270365
32	112.2	6.9	404	42	AI074921
33	109.8	6.7	234	47	AI535068
34	108	6.6	217	32	AA377893
35	64.2	3.9	467	29	AA127694
36	59.4	3.6	469	40	AA922128
37	56.6	3.5	107	27	AA014965
38	54	3.3	1056	26	W42205
39	51.2	3.1	641	45	AI357868
40	49.8	3.1	325	46	AA617058
41	49.8	3.1	376	46	AI433590
42	49.8	3.1	311	47	AI520908
43	49.4	3.0	759	26	W28277
44	49.2	3.0	238	25	W04550
45	49	3.0	196	38	AA766464

ALIGNMENTS

RESULT 1
LOCUS AA049280
DEFINITION m45d02.r1 Soares mouse embryo Nbmrl3.5 14.5 Mus musculus cDNA
RECEPTOR BETA CHAIN PRECURSOR
ACCSSSION AA049280
NID 91735311

464 bp mRNA
EST 30-DEC-1996
clone IMAGE:479043 5' similar to SW:rl6b MOUSE Q00560 INTERLEUKIN-6
RECEPTOR BETA CHAIN PRECURSOR ; mRNA sequence.

VERSION	AA049280.1	GI:1755311
KEYWORDS	EST	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 464)	
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,	
	Gessel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,	
	Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,	
	Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and	
	Waterston,R.	
TITLE	The WashU-HHMI Mouse EST Project	
JOURNAL	Unpublished (1996)	
COMMENT	On Dec 30, 1996 this sequence version replaced gi:1528951.	

Contact: Maria M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LINT; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:289787
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 437.
 Location/Qualifiers
 1..464

```

/clone="IMAGE:479043"
/clone_lib="Soares mouse embryo NIMEL3.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/notes="vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer 15',
TGTATCCATCTGAAGTGGAGCGCGCCGGAAATTTTCTTTTTTTTTTTTTTTT
T 3'g, on equal amounts of mRNA from 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 j]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT733 vector. Library was through one round of
normalization, and was constructed by Bento Soares and
M.Felina Bonaldo."

```

	Query Match	28.5%	Score 464	DB 29	Length 464
	Best Local Similarity	100.0%	Pred. No. 1e-79		
	Matches 464	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	557	gctgctgtgtccgcgaactgtgaagatcttcacgtgcgcgtgtgacaccgggtgcacacgggg			616
Db	1	gctgtgtgtgtccgcggaactgtgaagatcttcacgtgcgcgcgtgtgacaccgggtgcacacgggg			60
QY	617	agacattcttcatacatcaccaactactccctccaagtacaagctgtggtgtcatcagata			676
Db	61	agacattcttttaccatcccaactactccctccaagtacaagctgtggtgtcatcagata			120
QY	677	acacatgtgagagagatgacacacactgtgtgggcccctcatgatgcattcccccaaggactgtg			736
Db	121	acacatgtgagagagatgacacacactgtgtgggcccctcatgatgcattcccccaaggactgtg			180
QY	737	ccctcttcaactccctcatgatgatctgtgtgtgaaagcaccacaaatcgctctggtcttagcaaat			796

[illegible]

RESULT	2
M6776/c	
LOCUS	
DEFINITION	w6776 482 bp mRNA EST 14-JUN-1996 me17bl.1 r1 Soares mouse embryo; NbMw1.5 14.5 Mus musculus CDNA clone IMAGE:387741 5' similar to PIR:38252 B38252 granulocyte colony-stimulating factor receptor precursor ; , mRNA sequence.
ACCESSION	w6776
NID	g1375694
VERSION	G1:1375694

ORGANISM *Mus musculus*
Eukaryota: Metazoa: Chordata: Craniota: Vertebrata: Mammalia:
Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
REFERENCE
1 (bases 1 to 482)
AUTHORS Maria, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Gessel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Thausing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL
COMMENT Unpublished (1996)
On Apr 14, 1993 this sequence version replaced g1:785250.

Contact: Maira M/Mouse EST Project
 Wash-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LINT; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:339573
 Possible reversed clone; similarity on wrong strand
 Seq primer: EMP1mer
 High quality sequence stop: 359.
 Location/Qualifiers
 1..482

```

/strain="C57BL/6J"
/db_xref="taxon:10090"
/map="10 pter.cen"
/clone="IMAGE:387741"
/clone_id="Soares mouse embryo NBMEL3.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
/note="vector: pRT3D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I oligo(dt) primer [5',
TGTATCCATCTCAAGTGGAGCGCGCCGCAATATTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2

```

14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 96 a 138 c 147 g 101 t
ORIGIN

Query Match 28.1%; Score 457.8; DB 26; Length 482;
Best Local Similarity 99.4%; Pred. No. 1.6e-78;
Matches 470; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 664 tacggctcggagaaacacatgtgagagtaaccactgtggccctccaccatgcatatc 723
|||||
Db 482 TACGGCTCAGGATTAACATGTAGAGATCCACACTGTGGGCCCTCACACAGCCATATC 423
724 cccaaggaacctggccctcttcacatcctatgagatcgtggtaagccacaacatgccta 783
|||||
Db 422 CCAAGGACCTGGCCCTCTTACCTCCATAGATCTGGGTGGAAGCCCAATGCGCTA 363
784 ggcctcagaacatcctgagctcctcacaactgagctgctcgtgagacgtgtgacacagagcccc 843
|||||
Db 362 GGCCTCAGCAAGATCTGATGTCTCTCACACTGATGTCTGAGAGTGGTGACACGAGACCCC 303
844 ccaccagcagctgacagctgagcggctgtgggcccggagagacacactgagctgtgctggc 903
|||||
Db 302 CCACCCGACGTGACAGTGAAGCGCGCTGGGGCGCTGAGAGACCACTGATGTGGCGTGG 243
904 gtctcaccacacagcctcacaagatctcctctcacaagccaagtacag-atecgtacag 962
|||||
Db 242 GTCACACACACAGCTCTCAGAGATTTCTCTCCAGCAACCAATACCAATATTCCTACCG 183
963 cgtgagagacacgtgtgacatggaagtggtgagacgtctcagcaacacagacctctctgcg 1022
|||||
Db 182 CGTGAGAGACACAGCTGAGTGAAGTGTGTGATGACGTGACCAACACAGACTCTCTGCGG 123
1023 tctcggagccttgtaagcccgagaccttactctgtccaagtgtgttaaccatctgg 1082
|||||
Db 122 TCTGCGGGGCTGAAGCCCGGACACGTTACTCTCCCAAGGCGCTTGTAACCAATGCGG 63
QY 1083 gatcatgtgtcgaagaaagcgagacatctgagagagatgtggaagccacccacagc 1135
62 GATCATGTGCTGAAAAAGCGCGGAATCTGAGCGAGTGGAGCCACCCCATCG 10

RESULT 3
LOCUS AA866388 428 bp mRNA EST 05-FEB-1999
DEFINITION UI-R-A0-aj-f-04-0-UI.s3 UI-R-A0 Rattus norvegicus cDNA clone.
UI-R-A0-aj-f-04-0-UI.3 similar to gb|AC003112|AC003112 Human DNA
from chromosome 19 specific cosmid R30292, genomic sequence,
complete sequence (Homo sapiens), mRNA sequence.
ACCESSION AA866388
NID 54230568
VERSION AA866388.1 GI:4230568
KEYWORDS EST.
SOURCE Norway rat.
Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 428)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT On Mar 16, 1998 this sequence version replaced gi:2961849.

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping

University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: mesoares@blue.weeg.uiowa.edu
Oligo-dt track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA library preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics
Seq primer: M13 Forward.

FEATURES
source
Location/Qualifiers
1..428
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/map="between D1S1765 and UGR"
/clone="UI-R-A0-aj-f-04-0-UI"
/clone_1id="UI-R-A0"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; This library
consists of a mixture of individually tagged normalized
libraries constructed from rat placenta, adult lung,
brain, liver, kidney, heart, spleen, ovary, and muscle.
The tag is a string of 3-5 nucleotides present between the
Not I site and the Oligo-dt track which allows
identification of the library of origin of a clone within
the mixture."

BASE COUNT 87 a 134 c 120 g 87 t
ORIGIN

Query Match 24.1%; Score 391.8; DB 45; Length 428;
Best Local Similarity 94.8%; Pred. No. 6.5e-66;
Matches 405; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 659 ggtggtacggtcagagataacacatgtgagagtaaccactgtggccctcactatgac 718
|||||
Db 2 GCGCGCTCAATCAGAGACACACATGTGAGAAATACACACTGTGGCCCTCAGCTGCGC 61
719 atatcccaagagcctggccctctcactcctcctatgagatctgtgtggaagccacaatc 778
|||||
QY 719 atatcccaagagcctggccctctcactcctcctatgagatctgtgtggaagccacaatc 778
Db 62 ATATCCCAAGACCTGGCCCTCTTACCGCCCTATGAGATCTGGGTGGAAGCCACCATC 121
779 gctcagctcagcaagatctgagtctcctcacaactgagctgtcctcgtgagctgtgacacag 838
|||||
Db 122 GCGTGGGTTCAGCGAGATCTGACGTGCTCACTGATGATGCTGTGAGCTGTGATACCGG 181
839 accccaaccagcgtcagctgagcgcggtgtggggcctgtgagagacacagctgagtgtgc 898
|||||
Db 182 ACCCTCCACCCGACGAGTCACTGAGCCGCGTGGGGCGCTGAGAGACCACTGAGTGTGC 241
899 gctgggtctcaccacagcgtctcaagattctcctcctcacaagcaagttaccagatcgct 938
|||||
Db 242 GCTGGGTCTCACACACGCTCTCAAGATTCTCTTCCATCAAGCCAAATACAGATTGCT 301
959 acccgctgagagacagcgtgagctgagcaggtgtgtgagtgagctcagcaacacagacctct 1018
|||||
Db 302 ACCGCTGAGAGAGAGAGCTGAGCTGAGAGGTGTGATGAGCTGACGACCAAGACTCTCT 361
QY 1019 gcgctcgcggcgctgaagcccgacacgcttactctgtccaagtgcgtgtgaacctat 1078
|||||
Db 362 GCCGCTCGCGGCGCTTGAAGCCCGACCGCTTACTGTCACAGTCTGTTGTAACCAT 421
QY 1079 tcgggat 1085
|||||
Db 422 TCGGGAT 428

RESULT 4
LOCUS AI421423 474 bp mRNA EST 30-MAR-1999

```

DEFINITION
t125h01.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2097265 3
similar to SW:1168 MOUSE 000560 INTERLEUKIN-6 RECEPTOR BETA CHAIN
PRECURSOR ;, mRNA sequence.

ACCESSION
AF121423

NID
94267354

VERSION
AF121423.1 GI:4267354

KEYWORDS
EST.

SOURCE
human.

ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 474)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTCAP), Tumor Gene Index
(Unpublished (1998))

JOURNAL
COMMENT
On Apr 7, 1998 this sequence version replaced gi:304955.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
www-bio.llnl.gov/bbrp/imagenage/image.html

Insert Length: 1664 Std Error: 0.00
Seq Primer: -40UP from GIDCO
High quality sequence stop: 450.
Location/Qualifiers
1. 474
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2097265"
/clone_id="NCI-CGAP_Brn23"
/lisue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pRT3D-pac (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTATCCAAATCTGAAGTGGAGCGCGCCGCAATCTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pRT3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT
81 a 181 c 128 g 83 t 1 others

ORIGIN
Query Match 22.4%; Score 364.2; DB 46; Length 474;
Best Local Similarity 85.4%; Pred. No. 1.3e-60;
Matches 405; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

195 gtgcgcctgtgtgcctgtgtccctgtgctgggggtgctggggcgagatgagagcccaacagc 254
Db 1 GCCCTGTCTGCTGCTCTTCGCTCTCGGCGCGCGCGGACCGCGGATAGGAGGCCACACAGC 60

255 tgaatcagccccacagagcccccacccctctcatcagctctccctcgtcaaatctactgctc 314
Db 61 TGTGATCAGTCCGCCAGATCCACAGCCTTCTATATGGCTCTCTCCCTGCTGGCCACCTGCTC 120

315 tatacatgagacacacactgtgggacacgcgtgaggggtctactgtgacccctaatgctgc 374
Db 121 AGTGACGAGAGACCCACACAGGAGCCACCGCCGACGAGGCGCTCTACTGAGACCTCAATGGGCG 180

375 cgcgcctcctctgtgagcgtgccgcctctcttaaacctccacacccgcgcctcgtgcctggc 434

```

Db	181	CCGCGCTCCCCCTGAGACTCTCCCGGTACTCAAGCGCTCCACCTTGGCTCTGGCCCTGGC	240
Qy	435	taacctaatatggatccaggcagtcaggaagaacatctggtgtgtcacgcccgaagcg	494
Db	241	CACCTTAATATGGGATCAGGCAGCGTGGGGGCAACCTGATGGCAGCGCCGtgAGCG	300
Qy	495	cagcatctcgtcgtgcctcctcctactatgtctgtgcctccctgaagaagccctttaatc	554
Db	301	CAGCATCTCTGGCTGGCGTCCCTCTATGTGGCCCTGCCCCAGAGAAACCCGTAAACT	360
Qy	555	cagctgtgtgtcccgagaacataagaatctcaactgcgctgaaacagcggatgcaacag	614
Db	361	CAGTGTGTGGTCCAAAGAACATGAAGACTTGACTCGCTGGAGCCAGGGGCCACGG	420
Qy	615	ggaaacattttatataccaaactacccctccctcaagtcaacgctcgaggtgtgtaag	668
Db	421	NGAAGCTTCTCTCACACACAACTACTCCCTCAAGTACAAAGCTTAAGTGGTATGG	474

```

RESULT      5
LOCUS       A1185924
DEFINITION  A1185924, 477 bp, mRNA, EST, 29-OCT-1998
LOCUS       9550605.x1, Soares fetal_lung NBHL19W Homo sapiens cDNA clone
IMAGE       1142x408, 3', similar to TR:Q16354, Q16354 PROLACTIN RECEPTOR ;
RNA         mRNA sequence.
ACCESSION   A1185924
NID         93736562
VERSION     A1185924.1
KEYWORDS    GI:3736562
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 477)
AUTHORS    NCI-CCAG .
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     On Feb 17, 1998 this sequence version replaced gi:2150926.

```

FEATURES
 source
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 1552 Std Error: 0.00
 Seq primer: -40UP from Glbco
 High quality sequence stop: 467.
 Location/Qualifiers
 1. 477
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1742408"
 /clone_lib="Soares_fetal_lung_NbH19w"
 /dev_stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: lung; Vector: pTR73D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer
 [5'-GTTCACATCTGAAGTGGAGCGCCGACATTTTTTTTTTTT-3'
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pTR73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M. Fatima Bonaldo. This library was constructed
 from the same fetus as the fetal heart library, Soares
 fetal heart NbH19w."

```

source
1. 503
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:479046"
/clone_1ib="Soares mouse embryo NBMEL3.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand
CDNAs primed with a Not I - oligo(dT) primer [5',
TGTTCACATCTGAGTGGAGCGGCCCGCCGAAATTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ], double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Falima Bonaldo."
BASE COUNT      85 a      158 c      154 g      106 t
ORIGIN

Query Match      21.9%; Score 356.6; DB 29; Length 503;
Best Local Similarity 89.9%; Fred. 3.6e-59;
Matches 456; Conservative 0; Mismatches 4; Indels 47; Gaps 5;

QY 1055 tcgtccaaagtgtgtgtataccatcggatctatggttcgnaaaagccggaaatctga 1114
Db 503 TCGTCCAAAGTGGGTGTATAACCATTCGGGAGTATAGGCTCGAAAAGCGGGAATCTGGA 444
QY 1115 gcgagtgaagccaccaccacgcgtctctccaccctcgaagtgaagcgcggcgccggcg 1174
Db 443 GCGAGT-GAGCCACCCACACCCGCTGCTCACCCTCGAAGTGA-TGGCGGGCCCGGGGG 386
QY 1175 gcgagggtgtcgagccgcgggcgcgccgagctcgggccgggtgctggcgagctca 1234
Db 385 GCGGGGCTGTC-CGACGCGGGGGCGGCGA-CCAGCTCGGGCCCGGGTGGCGGAGCTCA 328
QY 1235 agcagctctcgcgtgtgtctcaagaagcagatactgtctgaacttgaatttcgcctgt 1294
Db 327 AGCAGTTCCTCGGCGGTCAAGAAAGCAGCATGCTGTCACACTTACCTTACCTTACCT 268
QY 1295 agcagccagtgccggtgtgtgtatgcagaagttcacacaagaccggaaac----- 1343
Db 267 ACGACCACTGCGCTGCTTGAATGACAGAAGTCAACACAAACCAGCAAGAGAGGGA 208
QY 1343 ----- agtccctccggtctaaacttaagatag 1371
Db 207 TCGTGCCTCGGCGAGAGGGGCTGCGCGAAGAGTCTGCGGCTTAACCTTAAGAGTAG 148
QY 1372 gcaatctctctgtgtgtcgaaccttggaaggtcacaactgaatttgagccctctaccat 1431
Db 147 GCGACTCTCTGCTGTGGGACAGACTGAGGCTCACTGGAATTGAGAGGCCCTCTTACCAT 88
QY 1432 ctgggcaacaagaacctactacagaaggtctggggcacaatgagctccacaacacagctt 1491
Db 87 CTGGGCAACAAGAAAGAACTTACCAAGAGCTGGGGCACAATGAGCTCCACAAACACAGACTT 28
QY 1492 tggtcacatgatgtgtcacacttgat 1518
Db 27 TGGTCCACATGATGTGTCACACTTGAT 1

RESULT 7
LOCUS      AI394468      462 bp      mRNA      EST      30-MAR-1999
DEFINITION      t179412.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105495 3',
MRA sequence.      AI394468
ACCESSION

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QY 195 gtagcgccttgtagcctctgtccctcgagggtccctcgaggcgagatcgggaagcccaacagc 254
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QY 255 tgtaacagaccccaagagaccaccccttcctatcgcgtctccctctgaagctaacctgtc 314
Db 61 ttgtgattcattcccaagattccacgccttctatgtggcctccctcctgtggcagacctctc 120
QY 315 tatacatgagagacacacactgaggccacgcgtgaaaggctactatgagacctcaatggtcg 374
Db 121 agtgcacggagagaccacacagagaccacgcgagggcctctatcgtgagacctcaatggcgc 180
QY 375 cgcgcctgcaccttgagctgtcccgacctcttaaacacctcaaacctcgagccctggcctcggc 434
Db 181 cgcctctggccccccttgaccttctccctgttactaacgcctctcacactgttgctctggccctggc 240

Query Match	21.7%	Score 354;	DB 43;	length 466;
Best Local Similarity	85.6%	Pred. No. 1.	1e-58;	

Db 181 CTACTGACCCCTAAGGGGCGCCCTGCCCTGAGCTCTCCCTGTAACAAGCCTC 240
 QY 414 caccctggcccttggccttgctactaattgggtccagcagcagcagcagcagcagc 473
 Db 241 CACCTTGGCTCTGGCCCTGGCCCAACCTCATGGGTCCAGGACCGGTGGGAGACAACCT 300
 QY 474 ggtgtgtcagcccgagcagcagcagcagcagcagcagcagcagcagcagcagc 533
 Db 301 CGGTGTCCACGCGCCCTGAGGGGAGCATCCGTGCTGCTCTCTCTATGTGGCTGCT 360
 QY 534 cccttgaagaccccttaaatcagctgctgctgctgctgctgctgctgctgctgctg 593
 Db 361 CCCAGAGAAACCCGTAACATCAGCTGTGCTCAAGAACATGAAGACTTGACCTGCC 420
 QY 594 ctggagaccgggtgacacagcgggagagac 620
 Db 421 CTGAGCGCCAGGGGCGCCACGAGAGAC 447

RESULT 12
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 LOCUS gp93el2.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
 DEFINITION IMAGE:1930606.3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR ;
 mRNA sequence.
 ACCESSION A133812
 NID 94070371
 VERSION A133812.1 GI:4070371
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 431)
 AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT On Jan 14, 1998 this sequence version replaced gi:1797892.

CONTACT: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1615 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 407.

FEATURES
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 /dev_stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: Lung; Vector: pT73D (Pharmacia) with a
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 strand cDNA was primed with a Not I - oligo(dT) primer
 [5'-GTATACCAATCTGAGTGGGAGCGGCGCAATTTTCTTTTCTTTT-3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo. This library was constructed
 from the same fetus as the fetal heart library, Soares
 fetal heart NbHL19W."

BASE COUNT 68 a 169 c 122 g 72 t
 ORIGIN

Query Match 19.9%; Score 324.2; DB 45; Length 431;
 Best Local Similarity 85.2%; Pred. No. 5.6e-53;
 Matches 362; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 198 gccctctgtgtctctgtctctgtctctgtctctgtctctgtctctgtctctgt 257
 Db 7 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 66
 QY 258 aatcagccccccaggaacccaccctctctctctctctctctctctctctctctat 317
 Db 67 GATCACTCCCGAGGATCCACGCTTCTCATCGCTCTCTCTCTCTCTCTCTCTCTCT 126
 QY 318 acatgagacacacccctgggagccgctgaggggctctactctgagccctcaatgagcgcg 377
 Db 127 GCAGGAGAGACCCACGAGGAGCCACGCGCCGCTCTACTGACCTTCAACGGGCGCG 186
 QY 378 cctgccccttgagctgtccgctctccttaccacccctcagccctgagccctgtctaa 437
 Db 187 CTGCCCCCTGAGCTCTCCGCTGTAACGCTTCAACGCTTGGCTTGGCTTGGCTTGG 246
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 Db 247 CCTCAATGGGTCCAGGACGCGCTCGGGGACAACTCGTGTCCACGCGCGTGAAG 306
 QY 498 cattctgtgctgctctgctctctctctctctctctctctctctctctctctct 557
 Db 307 CATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366
 QY 558 ctgctgtctccggaacatgaagatctcagctgctgctgagacccgggtgacagcggg 617
 Db 367 CTGCTGCTCCAGGAACATGAAGACTTGAACCTGCGCTGAGACCCGAGGCGCCAG 426
 QY 618 gacat 622
 Db 427 GACCT 431

RESULT 13
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 LOCUS q126b05.x1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:1857585
 DEFINITION 3', mRNA sequence.
 ACCESSION A1269388
 NID 93888555
 VERSION A1269388.1 GI:3888555
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 417)
 AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT On Aug 21, 1998 this sequence version replaced.

CONTACT: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1634 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 406.

FEATURES
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 /clone="IMAGE:1857585"
 /clone_lib="Soares_NbHMPu_S1"
 /tissue_type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Oligo-RT track not found. Not a site shown in beginning of sequence
is likely internal to the message. cDNA library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward.

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/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: PT733d-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-G0
library is a normalized library constructed from a
mixture of rat tissues (nodose ganglia, dorsal root
ganglia, and trigeminal ganglia). The tag is a string of
6 nucleotides present between the Not I site and the
cligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6:
91-806, 1996"
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BASE COUNT ORIGIN	46 a	116 c	88 g	68 t	1 others
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Query Match	17.58;	Score 284.4;	DB 48;	Length 319;
Best Local Similarity	93.18;	Pred. No. 2.2e-45;		
Matches 297; Conservative	0;	Mismatches 22;	Indels 0;	Gaps 0;

[illegible]

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466 gacaatctgtgtgtcacy 484
      |||||
301 GACAATCTGGTGTCTACG 319

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 28, 1999, 16:36:58 ; Search time 3489.95 seconds
(Without alignments)
1524.566 Million cell updates/sec

Title: US-09-037-657-14

Perfect score: 1673

Sequence: 1 ggcacgagcttcgctgcg.....aaaaaaaaaaaaaaaa

Scoring table: IDENTITY_NUC

Searched: 679419 segs, 1590154680 residues

Database: GenEmbl.*

1: gb_bal.*
2: gb_ba2.*
3: gb_om.*
4: gb_ov.*
5: gb_pat.*
6: gb_ph.*
7: gb_pl1.*
8: gb_pl2.*
9: gb_pl.*
10: gb_pr2.*
11: gb_pr3.*
12: gb_ro.*
13: gb_st.*
14: gb_sy.*
15: gb_sy.*
16: gb_un.*
17: gb_vl.*
18: em_fun.*
19: em_hg.*
20: em_hum1.*
21: em_hum2.*
22: em_in.*
23: em_om.*
24: em_or.*
25: em_ov.*
26: em_pat.*
27: em_ph.*
28: em_pl.*
29: em_ro.*
30: em_st.*
31: em_sy.*
32: em_un.*
33: em_vl.*
34: gb_hg1.*
35: gb_hg2.*
36: gb_in1.*
37: gb_in2.*
38: em_bal.*
39: em_ba2.*
40: em_hum3.*
41: em_hum4.*
42: gb_pr4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1673	100.0	1673	5	A70384	Sequence 14

2	1563.4	93.4	1629	5	A70382	A70382 Sequence 12
3	1346	80.5	1930	5	A70382	A70382 Sequence 22
4	1021.6	61.1	1716	11	AF059293	AF059293 Homo sapi
5	836.6	50.0	1391	5	A70394	A70394 Sequence 24
6	803.8	49.7	834	5	A70388	A70388 Sequence 18
7	452.8	27.1	560	5	A70393	A70393 Sequence 23
8	304	18.2	938	5	A70386	A70386 Sequence 16
9	280.4	16.8	6663	5	A70398	A70398 Sequence 28
10	280.4	16.8	11832	5	A70408	A70408 Sequence 38
11	221.8	13.3	40668	11	AC003112	AC003112 Human DNA
12	55.6	3.3	342379	34	CEX3986	295399 Canorthabid
13	53	3.2	7218	5	I66494	I66494 Sequence 14
14	51.2	3.1	15528	17	PEAVEN	I07862 Plasmid pA
15	49.8	3.0	248287	35	AC007225	AC007225 Homo sapi
16	48.6	2.9	168919	35	AC007686	AC007686 Homo sapi
17	48.6	2.9	985	10	HSGPLP	X53463 Human mRNA
18	48.6	2.9	3849	12	AF091457	AF091457 Rattus no
19	48.4	2.9	4974	11	AF029778	AF029778 Homo sapi
20	48.4	2.9	4860	11	AF029778	AF029778 Homo sapi
21	48.4	2.9	128989	34	AC005151	AC005151 Homo sapi
22	47.6	2.8	8089	1	STMDAUBCE	L34880 Streptomyce
23	47.4	2.8	41230	1	MTCT253	L34880 Streptomyce
24	47.2	2.8	1531	4	GGU37273	U37273 Gallus gall
25	47.2	2.8	1849	4	GGU5823	U95823 Gallus gall
26	47.2	2.8	1934	5	A49139	A49139 Sequence 1
27	47	2.8	1319	10	HSVHATPE	X76228 H.sapiens m
28	47	2.8	1438	36	DMU86867	U86867 Drosophila
29	46.8	2.8	438	3	S78251	S78251 growth horm
30	46.8	2.8	2161	12	MMU52842	U52842 Mus musculu
31	46.8	2.8	204263	35	AC007224	AC007224 Homo sapi
32	46.6	2.8	3580	11	AF038440	AF038440 Homo sapi
33	46.4	2.8	3553	10	HSPPLC	Z16411 H.sapiens m
34	46.4	2.8	115958	11	AC004736	AC004736 Homo sapi
35	46.4	2.8	1595	11	AF070528	AF070528 Homo sapi
36	46.2	2.8	2304	37	AF080675	AF080675 Dictyoste
37	46	2.7	1547	7	VYLSSTSM	X76892 V.vnifera
38	46	2.7	559	11	AF014955	AF014955 Homo sapi
39	45.8	2.7	6170	10	HSCGGE7	AJ001216 Homo sapi
40	45.8	2.7	183871	35	AC007365	AC007365 Homo sapi
41	45.8	2.7	1217	37	AF145633	AF145633 Drosophila
42	45.6	2.7	2394	11	AF061795	AF061795 Homo sapi
43	45.6	2.7	183249	42	AC004828	AC004828 Homo sapi
44	45.6	2.7	2472	42	AF151685	AF151685 Homo sapi
45	45.4	2.7	152261	17	HEICG	X14112 Herpes simp

ALIGNMENTS

RESULT	1	LOCUS	A70384	Sequence 14	1673 bp	DNA	PAT	07-MAR-1999
DEFINITION								
ACCESSION								
NID								
VERSION								
KEYWORDS								
SOURCE								
ORGANISM								
REFERENCE								
AUTHORS								

1 (bases 1 to 1673)
Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Meda, M. and Kikuchi, Y.
A NOVEL HEMOPOLYMER RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
Patent: WO 98/1225-A 19-MAR-1998;
NICOLA NICO ANTONY (AU)
Location/Qualifiers
1. 1673
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/db_xref="taxon:32644"

FEATURES
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BASE COUNT 344 a 550 C 474 G 305 T
ORIGIN

2.

[illegible]

[illegible]

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Db	1141	CTCCACCCCCTCGAATGTAGAGCCGCCGGGCCCGGGGGGGGTGTGCGAGCCGGGGCGG	1200
OY	1201	cgaagcagcgttcggccccgggtgtgcgcgcgaagctaagaagttcccgcgttgcataaaa	1260
Db	1201	CGAGCCCAAGCTCGGGCCCCGGGTGCGGCGAGCTCAAGAAGTTCCCTGGCTGCCTAAAGA	1260
OY	1261	gaagcatatagctctgaagaccttaatttcgcgcctgttagaccagatgagtgcttgatcca	1320
Db	1261	GCAGCATATAGCTCTGAAACTTAGTTTCGCCCTGTACGACCAAGTGCGCGCTGTGATCCA	1320
Db	1321	GAAATCACACAAGAACCCGAACCAAG	1346
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AF059293			
LOCUS	1716 bp	mRNA	PRI 02-AUG-1998
DEFINITION	Homo sapiens cytokine-like factor-1 precursor (CLF-1) mRNA,		
ACCESSION	complete cds.		
NID	AF059293		
KEYWORDS	g3372626		
SOURCE	AF059293.1 GI:3372626		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1716) Elson,G.C.A., Graber,P., Losberger,P., Herren,S., Gretener,D., Menoud,L.N., Wells,T.N.C., Kosco-Vilbois,M.H. and Gauchat,J.F. CLF-1, a Novel Soluble Protein Shares Homology With Members of the Cytokine Type-I Receptor Family J. Immunol. (1998) In press 2 (bases 1 to 1716) Elson,G.C.A., Graber,P., Losberger,P., Herren,S., Gretener,D., Menoud,L.N., Wells,T.N.C., Kosco-Vilbois,M.H. and Gauchat,J.F. Direct Submission Submitted (14-APR-1998) Dept. of Immunology, Seroo Pharmaceutical Research Institute, 14, Chemin des Aulx, Plan-les-Ouates, GE 1228, Switzerland		
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
FEATURES			
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PRLPVHRSRNGGLEDDLSVAMVSPRLKPEFLQAKTQILRIEDSVDRKVVDDVDSNPT
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DB	LOCUS	DEFINITION	ACCESSION	NID	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	BASE COUNT	ORIGIN
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Db	361	AACCTACTCCCTCAATACAAAGTGGAGGTGATCGGTCCGGATTAACACATGTGAGAGATTAC												
Qy	695	caactgttgagccctcaatcatatgcaatactcccaagagacccgtgacctcttaacccctat												
Db	421	CACACTGTGGGGGCCCATCTCATGCGCATTTCCCAAGACCTGGGCCCTTTACTTCCTAT												
Qy	755	gagatctgggtgaaagcccaaatcgccataagcttaagaagaatctgatatgtctcaactg												
Db	481	GAGATCTGGGTGGAAGCACCACCAATGCGCTAGGCTCAGCAAGATCTGATGTCTCACACTG												
Qy	815	gattgccttggaacgtgtgtacccaagagaccccccacccgaagtgcagtgagccgcttggtg												
Db	541	GATGTCTGGAGAGTGTGTACACACGAGACCCGCCACCGACGTGACAGTGAGCCGCGTTGGG												
Qy	875	gaccctggaggaacgaactgaatgtgtgtgtgtctcaaccacagatctcaaggattctctc												
Db	601	GCCCTGGAGAGACAGACTAGTGTGCGGTGGGTCTTCACACCAAGCTCTCAAGGATTCTCTC												
Qy	935	ttccaagccaagtacagaatccgtctaccgctgtggaaggaacagctgtgactgtgaagtgtg												
Db	661	TTCCAGACCCAAGTACCAATCCGATCCGCTACCGCGCTGGAGGACAGCGTGAATGGAGTGTG												
Qy	995	gattgccttggaacgaactctctgtccgtctctgagggccttgaagcccgacacggtttac												
Db	721	GATGACGTTCACCAACCAACACTCTCTGCGGTCTCCCGGGCCGGAAGCCCGCACCGCTTAC												
Qy	1055	ttcgtccaagctgctgtgtgaaccattctggaattctggaattgtgtgaaaaagggggga												
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RESULT	7													
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DEFINITION		A70393												
ACCESSION		94774671												
NID		A70393.1												
VERSION		GI:4774671												
KEYWORDS		unidentified.												
SOURCE		unclassified												
ORGANISM		unclassified												
REFERENCE		1. (bases 1 to 560)												
AUTHORS		Micola,N.A., Fabril,L., Farley,A., Nash,A., Willson,T., Rakar,S.,												
		Zhang,J.J., Alexander,W., Hllon,D.J., Kojima,T., Maeda,M. and												
		Kikuchi,Y.												
TITLE		A NOVEL HAEMOPHILIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME												
JOURNAL		Patent: WO 9811225-A 19-MAR-1998;												
		NICOLA NICOS ANTONY (AU)												
FEATURES		Location/Qualifiers												
source		1..560												
		/organism="unidentified"												
		/db_xref="taxon:32												

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Best Local Similarity	88.0%	Pred. No. 3.2e-85		
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QY	509	ggctcctgccttatgttgctcttgcgccccttgagaagcccttcaatcgcgcgtgtcc	568	
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Db	181	CACACCAACTCTCCCTCAAGTACAAAGCTTAGGTGATGAGCAGGACAAACACATGTAG	240
Oy	689	gaatgacacacacttggggccctcaatcatgtcgaatatcccaaggacctggcccttcaact	748
Db	241	GAGTACACACAGAGGGGGCCCCACTCTGTGCATATCCCAAGAGACTGGCTCTCTTTACG	300
Oy	749	ccctatgagatcttgggtgtgaagaccacaaatgcctgactgagctcagacaagatctgattctc	808
Db	301	CCCATGTAGACTCTGGGTGGAGGCCACCAACCGCCTTGCGTCCCGCTCCGATTTACTC	360
Oy	809	acactgtatctctctgaagctggtgtgaccacaagaccccccaacccagacgtgtcaagtgagccgc	868
Db	361	ACGGTGGATATCCCTGGATGTGTGTGACCAAGGAGACCCCCCGCCGAGGTGCACGTGAGCGC	420
Oy	869	gttgaggagccctggagggacagctgagtgtggcgtgtgtccaccacagctctcaagat	928
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Oy	929	tctctctccaagaccaaagtlacacagatccggtaccggtgtgagaaagcgtgtgactgaag	988
Db	481	TTCCCTTTTTCAGAGCAAAATACAGATCCGCTACCGAGTGTGAGACAAAGTGTGATGAGAG	540
Oy	989	gtgtgtgtgtgactgacgtcagcaa	1008
Db	541	GTGGTGGACGATGTGAGCAA	560

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RESULT      8
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DEFINITION Sequence 16 from Patent WO9811225.
ACCESSION  A70386
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VERSION  A70386.1
KEYWORDS  GI:4774665
SOURCE
ORGANISM  unidentified.
          unidentified
REFERENCE  1 (bases 1 to 938)
          Nicola,N.A., Fahl,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
          Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
          Kikuchi,Y.
TITLE  A NOVEL HAMPOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
JOURNAL  Patent: WO 9811225-A 19-MAR-1998;
        NICOLA NICOS ANTONY (AU)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 3..9e-54;
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Db 301 CAGG 304
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DEFINITION Sequence 28 from Patent WO9811225.
ACCESSION A70398
NID 94774676
VERSION A70398.1 GI:4774676
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified
REFERENCE 1 (bases 1 to 6663)
AUTHORS Nicole,N.A., Fabril,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
TITLE A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
JOURNAL NICOLO NICOS ANTONY (AU)
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Location/Qualifiers
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/db_xref="taxon:32644"
BASE COUNT 1462 a 1852 c 1715 g 1634 t
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Best Local Similarity 99.6%; Pred. No. 3,2e-49;
Matches 281; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION Sequence 38 from Patent WO9811225.
ACCESSION A70408
NID 94774683
VERSION A70408.1 GI:4774683
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified
REFERENCE 1 (bases 1 to 11832)
AUTHORS Nicole,N.A., Fabril,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
TITLE A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
JOURNAL NICOLO NICOS ANTONY (AU)
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Location/Qualifiers
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Matches 281; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 11
LOCUS AC003112/c 40668 bp DNA PRI 21-NOV-1997
DEFINITION Human DNA from chromosome 19 specific cosmid R30292, genomic
sequence, complete sequence.
ACCESSION AC003112
NID 92636669
VERSION AC003112.1 GI:2636669
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS 1 (bases 1 to 40668)
Lamerdin,J.E., McCreedy,P.M., Adamson,A.W., Burkhart-Schultz,K.,
Gordon,L., Christensen,M., Kyle,A., Ramirez,M., Stillwagen,S.,
Garnes,J., Danganan,L., Bruce,R., Quan,G., Montgomery,M., Ow,D.,
Kobayashi,A., Olsen,A.O. and Carrano,A.V.

TITLE Sequence analysis of an -1 Mb region containing the KEF2B gene in 19p12

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 40668)

AUTHORS Lamerdin,J.E.

JOURNAL TITLE Direct Submission

Submitted (21-NOV-1997) Human Genome Center, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA

FEATURES

source

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/organism="Homo sapiens"

/db_xref="taxon:9606"

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/chromosome="19"

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/cell_line="5HL2-B"

/clone_lib="LL19NC03 R chromosome 19 cosmid library"

/note="LL19NC03 cosmid library constructed at LLNL from flow-sorted chromosomes from hybrid 5HL2-B, which carries chromosome 19 as its only human chromosome."

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misc_feature

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misc_feature

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LRR

2257. 8516

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/note="HERV9 retroviral sequence"

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5425. .5722

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repeat_region

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repeat_region

complement(7505. .7783)

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8951. .9254

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9358. .9535

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misc_feature

complement(9629. .9672)

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/rpt_family="Alu"

10409. .10548

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misc_feature

10643. .10725

/note="predicted exon, program: grail2exons_human_1.3, frame: 1, quality: excellent, score: 100.000--DSS similarity to AA047548 zfi5e02.r1 Soares fetal heart NBH19W Homo sapiens cDNA clone 377018 5' (139. .221); 100% identity. --DSS similarity to AA136115 zK9D04.r1 Soares pregnant uterus NBHPU Homo sapiens cDNA clone 490063 5' (111. .192); 99% identity. --DSS similarity to AA452628 zX33f04.r1 Soares total fetus NB2HF8 9w Homo sapiens cDNA clone 788287 5' (83. .165); 100% identity. --DSS similarity

misc_feature

11127. .11331

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repeat_region

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misc_feature

complement(13756. .14029)

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complement(14100. .14672)

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misc_feature

15713. .15760

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NID 92724471
VERSION. I66494.1 GI:2724471

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 7218)
TITLE Dörner, F., Scheiflinger, F. and Falkner, F. Gunter.
JOURNAL Recombinant fowlpox virus
FEATURES Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
1. 7218
source /organism="unknown"
BASE COUNT 1944 a 1491 c 1486 g 1929 t 368 others
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Matches 8; Conservative 225; Mismatches 150; Indels 0; Gaps 0;

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Db 1111 YTY 1170
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QY 213 gtcctcgcgggtgcctcgcggcgagcgagccacacagctgtacagcccccag 272
Db 1231 YTY 1290
QY 273 acccaaccttcacatcgctcctccctcgaactacactgctctatatacgagacac 332
Db 1291 YTY 1350
QY 333 ctggggcgcccgctgagggcgccctactgacacctcaatgctcgccgctcgccctgagc 392
Db 1351 YTY 1410
QY 393 tgcctccgctccttaacacctcc 415
Db 1411 YTY 1433

RESULT 14
PEAVGEN 15528 bp mRNA VRL 29-JAN-1998
LOCUS PEAV030 containing cDNA of Equine arteritis virus, complete
DEFINITION genome.
ACCESSION Y07862
NID 91835169
VERSION 1
Y07862.1 GI:1835169
KEYWORDS GI gene: glycoprotein; Gs gene: membrane protein; nucleocapsid
protein; ORF1a; ORF1b; ORF3; ORF4; replicase; replicase
polyprotein; ribosomal frameshift signal.
SOURCE Equine arteritis virus.
ORGANISM Equine arteritis virus.
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Arteriviridae; Arterivirus.
REFERENCE 1 (bases 1 to 15528)
AUTHORS van Dinten, L.C., den Boon, J.A., Wassenaar, A.L., Spaan, W.J. and
Snijder, E.J.
TITLE An infectious arterivirus cDNA clone: identification of a replicase
point mutation that abolishes discontinuous mRNA transcription
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (3), 991-996 (1997).
MEDLINE 97175715
REFERENCE 2 (bases 1 to 15528)
AUTHORS Snijder, E.J.
TITLE Direct Submission

JOURNAL Submitted (10-SEP-1996) E.J. Snijder, Dept. of Virology, Institute
of Medical Microbiology, Leiden University, AZL Building 1, Room
P4-26, Postbus 9600, 2300 RC Leiden, NETHERLANDS
COMMENT Related sequences: X53459, X52275, X52276, X52277 & A02710.
FEATURES Location/Qualifiers
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ACCESSION AC007225
NID 94367163
VERSION AC007225.1 GI:4567163
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Jones, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D.,
Bryant, J., Tesmer, J., Meinkel, L., Longmire, J., White, S., Tatum, O.,
Campbell, C., Fawcett, J., Maltbie, M., Bussod, M., Sutherland, R.,
Han, C. and Deaven, L.
TITLE
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 248287)
AUTHORS Rhee, D.O.
TITLE Large Scale Sequence Analysis and Annotation with the Sequence

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RESULT      2
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AC          V41688;
DE          Nucleotide sequence of the murine U4 gene.
DT          26-OCT-1998 (first entry)
KW          Murine; U4 protein; haematopoietin receptor superfamily;
            cell proliferation; immune response; antibody; cell differentiation;
            autoimmune disease; cancer; allergy; ds.
OS          Mus sp.
FT          Key
FH          Location/Qualifiers
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PN          WO98331811-A1.
PT          23-JUL-1998.
PF          15-JAN-1998; U000334.
PR          16-JAN-1997; US-784863.
PA          (GENEY ) GENETICS INST INC.
PI          Collins M, Donaldson DD, Neben T, Whitters M;
DR          WPI; 98-414109/35.
P-SDSDB: W59804.
PT          New nucleic acid encoding U4 haematopoietin receptor superfamily
FR          chain - potentially useful, e.g. for modulating cell proliferation
PT          or immune response, for treating cancer and auto-immune disease
PS          Claim 1; Pages 25-26; 38pp; English.
CC          This is the nucleotide sequence encoding the murine U4 protein from
CC          the hematopoietin receptor superfamily, used in the method of the
CC          invention for the modulation of cell proliferation, or the immune
CC          response. Transformed mammalian cells are used to produce recombinant
CC          U4 protein. The U4 protein is used to screen for specific binding
CC          agents, raise antibodies. It is also used as reagents for assays and
CC          as tissue markers for isolation of cognate ligands and receptors, and
CC          in pharmaceutical compositions which may modulate cell proliferation,
CC          cell differentiation, and the immune system (e.g. for treating immune
CC          deficiency, inherited or the result of infection, autoimmune diseases,
CC          cancer, and allergy).
SO          Sequence 1656 BP; 318 A; 552 C; 478 G; 308 T;

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CC a cytokinln-like receptor. Soluble Zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thymoid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible Zcyto5 ligands. A probe
 CC comprising Zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcyto5 and
 CC therapeutically to modify Zcyto5 ligand effects.
 CC Sequence 1724 BP; 350 A; 550 C; 500 G; 324 T;

Query Match 84.9% Score 1421; DB 1; Length 1724;
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 DB 40 CGGCGTCCGCTGCGCGCCGAGTGAAGCGTGGGAGCCCAATCGACCC 99
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 CC |||||||
 DB 1539 GGGGCTGGGGGACATGAGCTCCACACACACACACACACACACACAC 1597
 QY 1555 gataaccacagctggtgtaagctg-----gggtatcagggcctccaa 1606
 CC |||||||
 DB 1598 GATGTACCCCAATATGGGTAGGGTGAAGTATGACAAAGGTTATGCA 1657
 QY 1607 caatctttaataat-----aagagattgttcagcaaaaaaaaaaaaaa 1662
 CC |||||||
 DB 1658 GAGTCTTTGAATTAATAGAAAAGATTGTTCAGGAAAAAATAAATAA 1716

RESULT 5
 V27158
 V27158 standard; DNA; 1930 BP.

AC V27158;
 DT 29-SEP-1998 (first entry)
 DE Unspliced murine NR6 nucleotide sequence.
 KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
 KW cell survival; therapeutic; neuronal proliferation; drug screening; ss;
 OS Mouse.
 PN Mus sp.
 OS WO9811225-A2.
 PD 19-MAR-1998.
 PE 11-SEP-1997; G02479.
 PR 11-SEP-1996; AU-002246.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA (DIE/) DIELEWSKA H E.

Query Match	60.58;	Score 1012.2;	DB 1;	length 1690;
Best Local Similarity	86.58;	Pred. No. 6.3e-201;		
Matches 1132; Conservative	0;	Mismatches 168;	Indels 9;	Gaps 1.

Db	801	GGACCACTAGAGCTGGCGCTGGGTGTCGCCACCCGCCCTCAGATTCTCTTTCACG	860
OY	943	CAAGTACCAGATCCGCTACCGCGTGGAGGACAGCTGAGTGAAGTGTGTGATGAGT	1007
Db	861	CAATATACCAGATCTCGCTACCGAGATGGAGGACATGTGTGACTGGAAAGTGTTGAGAGAT	920
OY	1003	CAGAACCAAGACCTCCGCTGCTGTGCGGAGCCCTGGAAGCCCGGACCGTTTAACTGTCGA	1067
Db	921	GAGCAACCAAGACTCTGCGCGCTGGCCGTGGCCCTCGAAACCCGGACCGCTATTGTTGTGA	980
OY	1063	AGTGCCTGTAAACCAATCTGAGTATCTATGTGTCGAAAGAGCGAGATCTGAGCGAGT	1122
Db	981	AGTGCCTGTAAACCCCTTTTGGCATCTATAGGCTCCAGAAAGCCGGGATGTGACGTAGTG	1046
OY	1123	GAGCGACCCCAACCGCTGCGCTCAACCCCTCGAAGTGAAGCGCCGAGCGCGGCGAGT	1187
Db	1041	GAGCGACCCCAACCGCGCTCTCACTCCCGCGAATGAGCCCGCGGCGCCGCGCGGGCG	1100
OY	1183	GTGCGAGCGCGGAGCGAGCGAGCCAGCTCTGGGCCGCTGCGCGCGAGCTTAACCACT	1247
Db	1101	GTGCGAATCCCGGGCGGAGAGCGCGAGCTCTGGGGCCGGTGGCGCGAGCTTAACCACT	1166
OY	1243	CGTCGAGTGTCTAAAGCAAGCAATCGCTCGAAGCTTAGTCTTCGACTGTACGACCA	1307
Db	1161	CGTGGGTGGCTCTAAGAAAGCAAGCGTATGCTCCAACTCAACCTTCCCTCTTACGACCA	1220
OY	1303	GTGCGTGTCTGTGATCTCAGAAATCAACAAGACCCGAAACCGAGCGAGAGTATCTCTGC	1362
Db	1221	GTGCGAGCTGTGATCTCAGAAATGCGCAACAAGACCCGAAACCGAGCGAGAGTATCTCTGC	1280
OY	1363	TTGCGGCAAGCGGAGTGTGCGGCGAAGAGTCTCTCTCGTGTAACTCTAAG	1411
Db	1281	CTGCGGCAAGCGGAGCGAGCGCGAGAGTCTCTCCAGAAATGCTGTAGGG	1329

	RESULT	7
ID	V70895	
AC	V70895 standard; cDNA; 1813 bp.	
DT	17-MAR-1999 (first entry)	
DE	cDNA encoding an allelic variant of human Zcytoz5.	
KW	Zcytoz5; cytokinin-like receptor; down-regulation; growth factor;	
KM	maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;	
KW	cardiac pathology; heart enlargement; zcytoz5 ligand; allelic variant;	
OS	ss.	
FH	Homo sapiens.	
FT	key	Location/Qualifiers
FT	CDS	88..1365
PN		/*tag= a
PD		/product= zcytoz5
PA	W09849307-A1.	
PF	05-NOV-1998.	
PR	01-MAY-1998; U08865.	
PR	13-FEB-1998; US-074721.	
PR	01-MAY-1997; US-045287.	
PR	01-MAY-1997; US-850030.	
PR	13-FEB-1998; US-023890.	
PI	(ZIMO) ZYMOGENETICS INC.	
PI	Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,	
PI	Lok S, Presnell SR, Whitmore TE;	
DR	WPI; 99-034662/03.	
DR	P-PsDB; W70861.	
PT	New mammalian cytokinin-like receptor Zcytoz5 - useful for, e.g.,	
PT	down-regulating Zcytoz5 natural ligands or detecting cardiotoxin-1	
PT	in blood	
PS	Disclosure: Page 68-70: 55pp: English.	
CCC	The present sequence encodes an allelic variant of protein designated	
CCC	Zcytoz5, which is a cytokinin-like receptor. Soluble Zcytoz5 may be	
CCC	administered to down-regulate the effects of a growth and/or maintenance	
CCC	factor in thyroid, heart, and skeletal muscle for example to lessen the	
CCC	effect of cardiotoxin-1 on cardiac pathologies, so preventing heart	
CCC	enlargement. Zcytoz5 could be used to detect cardiotoxin-1 in the	
CCC	blood, and to discover other possible Zcytoz5 ligands. A probe	

D	b	923	ACAGTGTGAGATCGAAGTGCTGTGGACGATGTGGACAAACCAACCAACCTCCGTGCCGCTGGCCG	982
Q	y	1032	gcctgaagcccccgcgacccgttacttcgtccaagtgcgttgtaeccattcggatcttg	1091
D	b	983	GCTTAAGACC GGCGCACCTGTACTTCGTGCAGAGTGCCTGCACACCCCTTTGGCATCTATG	1042
Q	y	1092	gtctgaaaaaggcgagaaatcttggagcgagttagaccaccaccaacgcgtctctcacccctc	1151
D	b	1043	GCTCCAAAGAAGCCGGGATCTGGAGTAGTGAGGACACCCACACGCCGCTTCATCCTCCC	1102
Q	y	1152	gaagtcgagccgcccgagcccgagcgaggtgtgtcgagaccgcgagggcgcgagcccaagt	1211
D	b	1103	GCAGTGACACGCCGGGGCCCCGGGGCGGGGGCTGCGAACCCGGGGGGGAGACGGCAGCT	1162
Q	y	1212	cgggcccgtgtcgcgcgagctcaaacagttccctgcgtgtgctcaagaagccgcatact	1271.
D	b	1163	CGGGGCGCGGTGGCGCGCGGCTCAAGCAGATTCTTGCGCTGCTCAAGAAGCACGGGTACT	1222
Q	y	1272	gtctgaaccttagttcttcgcgcgttcagccagtagtcgtgtcgagtcgaaagtcacaca	1331
D	b	1223	GCTCCAACTCAGCTCTCGCTCTACAGCAATGGCGAECTTGATGCAAGAGTCCGACA	1282
Q	y	1332	aacaccggaac-----caagacgagggagatccctgccttcgagcagaaggggtgcgagag	1386
D	b	1283	AACCCCGACACACAGCAGCAGAGAGAGGAGATCTGCGCCTGGGCGAGACGGGGCAG	1342
Q	y	1387	aggtctcgcgcggttaaactctaagg	1411
D	b	1343	AGGTCCTGCCAGATAAGCTGTAGGG	1367
R	E	S	U	L
I	D	V	A	1689
A	C	V	A	1689;
D	T	26-OCT-1998	(first entry)	
N	D	E	Nucleotide sequence of the human U4 gene.	
K	M	H	Human; U4 protein; haematopoietin receptor superfamily;	
K	M	cell proliferation; immune response; antibody; cell differentiation;		
K	M	autoimmune disease; cancer; allergy; ds.		
O	S	Homo sapiens.		
F	H	Key	Location/Qualifiers	
F	T	CDS	1..1228	
F	T		/tag="a	
F	T		/product="U4 protein"	
P	N	MO9831811-A1.		
P	D	23-JUL-1998.		
P	F	15-JAN-1998; U00334.		
P	R	16-JAN-1997; US-784863.		
P	A	(GENE) GENETICS INST INC.		
P	I	Collins M, Donaldson DD, Neben T, Whittens M:		
D	R	WPI: 98-414109/35.		
D	R	P-SDB: W59805.		
P	T	New nucleic acid encoding U4 haematopoietin receptor superfamily		
P	T	chain - potentially useful, e.g. for modulating cell proliferation.		
P	T	or immune response, for treating cancer and auto-immune disease		
C	C	Claim 1: Page 28; 38pp: English.		
C	C	This is the nucleotide sequence encoding the human U4 protein from		
C	C	the haematopoietin receptor superfamily, used in the method of the		
C	C	invention for the modulation of cell proliferation, or the immune		
C	C	response. Transformed mammalian cells are used to produce recombinant		
C	C	U4 protein. The U4 protein is used to screen for specific binding		
C	C	agents, raise antibodies. It is also used as reagents for assays and		
C	C	as tissue markers for isolation of cognate ligands and receptors, and		
C	C	in pharmaceutical compositions which may modulate cell proliferation,		
C	C	cell differentiation, and the immune system (e.g. for treating immune		
C	C	deficiency, inherited or the result of infection, autoimmune diseases,		
C	C	cancer, and allergy).		
S	Q	Sequence	1579 Bp; 304 A; 535 C; 473 G; 267 T;	

Query Match 58.8%; Score 984.2; DB 1; Length 1579;
Best Local Similarity 87.2%; Pred. No. 3.8e-195;

Db 181 AACCCTGATCATGAGTGTGTCACAGATGAGACTGACCTGCCGTGACG 240
 Qy 602 ccggatgcaacaggagagacattcttaccactactcccttaagttaagctagg 661
 Db 241 CCAGGGGCCCCAGGGAGAGCTCTCCACACCACTACTCCCTCAAGTACAGCTTAGG 300
 Qy 662 tggatcagctgagataacacatgtgagagtagtaccacactgtggccctcaatgacat 721
 Db 301 tggatgagccagagacacacatgtgagagtagtaccacactgtggccctcaatgacat 360
 Qy 722 atcccaagagactggccctcttcaactccctatgagatctgggtggaagcccaatgcg 781
 Db 361 ATCCCAAGAGACTGGCTCTCTTACGCCCTATGAGATCTGGGTGAGGCCACCAACCCG 420
 Qy 782 ctgagctcagcaagatctatgtctcccaacactggatgtctctggaagtggtgagcag 841
 Db 421 CTGGGCTCTGCGCTCCATGATGATCAAGTGAATCTGATGATGATGATGATGATGATG 480
 Qy 842 ccccccacccagctgacgtgagcgcgttgggggctggagagacagctgagtgagc 901
 Db 481 CCCCCCGGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGAC 540
 Qy 902 tgggtctacacacacagctctcaagattctctcttcccaagcccaagtaacagatcgctac 961
 Db 541 TGGGTGTCGCGCACCGCCCTCAAGATTCCTCTTCAAGCCCAATACAGATCCGCTAC 600
 Qy 962 cgcgtgagagacagcgtgagcgtgagagtggtgagtgagtgagtgagtgagtgagtgag 1021
 Db 601 CGAGTGAAGACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 660
 Qy 1022 cgcgtgagagacagcgtgagcgtgagagtggtgagtgagtgagtgagtgagtgagtgag 1081
 Db 661 CGAGTGAAGACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 720
 Qy 1082 gggatcattggtgagaaagcggagatctggagcagtgagagccacccacagctgtgc 1141
 Db 721 GGATCTATGATGCTCAAGAAAGCCGGAGATCTGAGTGTGAGTGTGAGTGTGAGTGTGAG 780
 Qy 1142 tccacccctcgaagtgagcgcggcgagcggcgagcggcgagcggcgagcggcgagcggcgag 1201
 Db 781 TCACCTCCCGCAGTGAAGCGCCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGG 840
 Qy 1202 gaggcagcagctggcgagcggcgagcggcgagcggcgagcggcgagcggcgagcggcgagcggcgag 1261
 Db 841 GAGCCGAGCTGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
 Qy 1262 cagcactactgctgaacactagttccgcctgtacgacagcagtgagtgagtgagtgagtgag 1321
 Db 901 CACCGTACTGCTCCAACTCAGCTTCGCGCTTACGACGAGTGGCGAGCTGATGACAG 960
 Qy 1322 aagtaacacagacccggaac-----caggaagagggagatctctctcgggagagaggg 1376
 Db 961 AAGTCGACAGACCCGACACACGACGAGGAGGAGATCTCCCTCGGGCAGAGCGG 1020
 Qy 1377 gtgagagagaggtctctgctgggttaacttaag 1411
 Db 1021 GCAGCGGAGAGTCTCCAGATTAAGCTGTAGG 1055

RESULT 10 V27143

V27143 standard: cDNA: 834 BP.

AC V27143.
 DE 29-SEP-1998 (first entry)
 KW Nucleotide sequence of products generated by 5N race of brain cDNA.
 KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
 KW cell survival; therapeutic; neuronal proliferation; drug screening; ss;
 KW Mouse.
 OS Mus sp.
 FH Key
 FT CDS
 Location/Qualifiers
 1..834
 /tag= a
 /product= "Haemopoietin receptor"

PN W09811225-A2.
 PD 19-MAR-1998.
 PE 11-SEP-1997: G02479.
 PR 11-SEP-1996: AU-002246.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 FA (DIE/) DZIELEWSKA H E.
 PI Alexander W, Fabril L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Mada M, Nash A, Nicola NA, Rakar S, Wallison T,
 PI Zhang J.
 DR WPI: 98-260970/23.
 DR P-PSDB: M55014.
 PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PT e.g. neuronal cells
 PS Claim 7: Page 93-95: 182pp: English.
 CC The nucleotide sequence was generated by a 5N RACE of brain cDNA using
 CC NR6 specific primers. NR6 is a novel Haemopoietin receptor (HR).
 CC Interaction between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and it's
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 834 BP: 167 A; 274 C; 225 G; 168 T;

Query Match 49.7%; Score 830.8; DB 1; Length 834;
 Best Local Similarity 99.8%; Pred. No. 1.8e-163;
 Matches 832; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 275 cccacccctctatcgagcctccctcgaagctgctctatcatatgagacacacact 334
 Db 1 CCCACCTCTCATGCGCTCCCTCCGACGATGCTGATATACATGAGACACACT 60
 Qy 335 ggggacacagctgaggggctctactgagacccaatggtccgcgcctcctcgtgagc 394
 Db 61 GGGGACACCGCTGAGGGGCTTACTGACCCCTCAATGATGCGCGCTGCTGAGCTG 120
 Qy 395 tcccgctccttaacacccctcgcgcctcggccttgctgaacttaagtgtccag 454
 Db 121 TCCCGCTCTCTTAACACCTTCACCTGCGCTGCGCTGCTGCTTAATGGGTCAAG 180
 Qy 455 cagcagtcagagagacatctgtgttcaagcggcgagagcagcattctgagctgctcc 514
 Db 181 CACCACTCAGAGACAAATCTGCTGTACGCCGACGACGACGACGATTCGGTGGCTCC 240
 Qy 515 tgcctatagtgtctgccccctgagagcccttaacatcaagctgtgtgtccggagac 574
 Db 241 TGCCTATGTTGGCTTGGCCCCCTGAGAACCTTTAATCACTGCTGTGCTCCGGAAC 300
 Qy 575 atgaagatctcaagctgtgcgtgtgagacgggtgtgacacggggagagatcttaacatcc 634
 Db 301 ATGAAGATCTCAAGTGGCCCTGACACCGGGTGCACACGGGAGATCTTACATACC 360
 Qy 635 aactacccctcaagtaacagctgagtggtgtacggtcagagataacacatgtgagagtag 694
 Db 361 AACTACTCTCTCAAGTCAAGCTGAGTGTGATGATGATGATGATGATGATGATGATGATG 420
 Qy 695 cacactgtggccctcactcatgcatatcccaagagacgtggccctctcaactccat 754
 Db 421 CACACTGTGGGGCCCCCATGTCATGCAATATCCCAAGAGACTGGCCCTTACACCTTAT 480
 Qy 755 gagatcgggtgtgagagcccaatcgctgtgctcgaagaagatctgtgtctcaactg 814
 Db 481 GAGATCTGGGTGTGAAGCCACCAATCGCTAGGCTCACCAAGATGTGATGCTCACACTG 540
 Qy 815 gatgctgtgagctgtgtgacagagaccccccacccagcagctgtgagagcgggtgag 874
 Db 541 GATGCTGTGAGCTGTGTGACACGACGACCCCCACGACGACGACGACGACGACGACGACG 600
 Qy 875 ggcctgtgagagcagcagctgagtggtgagtggtgtcaccacacagctctcaagattctc 934

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Db 601 GGGCTGGAGGACCTAGTGTGGCTGGCTCAGCCAGCTCTCAAGATTCTCTC 660
Qy 935 ttccaagcaagttaccagatccgctaccgcgctggaagagagtgagtgagtg 994
Db 661 TTCCAGGCAACTACCAATCCGCTACCGCTGAGAGAGAGGTGAGAGGAGTG 720
Qy 995 gatgagctgaagcaaacagactcctcctcctcctcctcctcctcctcctc 1054
Db 721 GATGAGCTGAGCAACAGACCTCTCGCGCTGCGGGGCTGAAGCCGCGCAT 780
Qy 1055 ttctgccaagtgctgtgacacccattcggatctatggctgaagaaagcgg 1108
Db 781 TTGCGCAAGTGCGTTGTAACCATTCGGGATCTATGGGTGAGAAAGCGGGA 834

RESULT 11
V27159
ID V27159 standard; DNA: 560 BP.
AC 29-SEP-1998 (first entry)
DE PCR product for human NR6
KW Hemopoietin receptor; cell proliferation; cell differentiation; cancer;
cell survival; therapeutic; neuronal proliferation; drug screening; ss;
Human.
OS Homo sapiens.
PN WO9811225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI (DZIE/) DZIELEWSKA H E.
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Meada M, Nash A, Nicola NA, Rakar S, Willson T,
PI Zhang J.
DR WPI: 98-260970/23.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PS Disclosure: Page 101: 182pp; English.
CC NR6 is a novel haemopoietin receptor (HR). Interaction between the novel
CC HR and a ligand facilitates proliferation, differentiation and survival
CC of a wide variety of cells. The HR and its derivatives can be used for
CC modulating the activity of the receptors e.g. to regulate development,
CC maintenance or regeneration in an array of different cells and tissues in
CC vitro and in vivo. They can be present in therapeutics used for
CC modulating neuronal proliferation, differentiation and survival. The
CC products can also be used for detection and diagnosis, e.g. for cancers
CC or predisposition to cancers, or for drug screening.
SQ Sequence 560 BP; 113 A; 182 C; 165 G; 100 T;

Query Match 27.1%; Score 452.8; DB 1; Length 560;
Best Local Similarity 88.0%; Pred. No. 2.4e-85;
Matches 493; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 449 tccagagcagctagtagagacaactgtgtgtcaagcccgagagcagcattctgct 508
Db 1 TTCAGGAGCGGCTGGGGGCAACCTCTGTGCAACGCCCTGTGAGGCGAGATCTCTGCT 60
Qy 509 ggcctcgcctctatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 568
Db 61 GGCCTCGCCTCTATGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Qy 569 cgaagacatgaagatctcaagctgcgcctgagacacgaggtgacacagggagacattctta 628
Db 121 AAGAACATGAGAGGACTTGACTCGCGCTGAGACGAGGCGCCACAGGAGACCTCTCTC 180
Qy 629 catccacactactccctcaagtaagtgagtgagtgagtgagtgagtgagtgag 688
Db 181 CACACCAACTACTCTCCCAAGTACAGCTTAGGTAGGTAGGCTGAGGAGACACACATGTGAG 240
Qy 689 gagacacacactgtggggccctcactcatatccccaaggaactgtgccccttact 748

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Db 241 GAGTACACACAGTGGGGCCACCTCTGCCACATCCCAAGAGACTGCTCTTACG 300
Qy 749 ccctatgagatctgggtggaagcccaatcgctaggctcagcaagatctgattcttc 808
Db 301 CCTATGATGATGTGGGTGAGAGCCACCAACCGCTGAGCTGTGCCCCCTCGAGTACTC 360
Qy 809 acactggtgtctctgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 868
Db 361 ACGCTGATTCCTGAGTGTGAGTACACAGACCCCGCCCGAGTGTGACGTAGCCGC 420
Qy 869 gtgggggcttggaagacagctgagtgagtgagtgagtgagtgagtgagtgag 928
Db 421 GTGGGGGCTCTGAGAGACCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 929 ttctcttccaagccaagttaccagatccgctaccgcgctggaagagagtgagtgag 988
Db 481 TTCTTTTTCAGCAAAATACAGATCCGCTACGAGTGGAGACAGTGTGATGAGAG 540
Qy 989 gtgtgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1008
Db 541 GTGTGAGAGTGTGAGCA 560

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RESULT 12

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V27142
ID V27142 standard; DNA: 938 BP.
AC 29-SEP-1998 (first entry)
DE Novel haemopoietin receptor NR6.3 gene.
KW Hemopoietin receptor; cell proliferation; cell differentiation; cancer;
cell survival; therapeutic; neuronal proliferation; drug screening; ss;
Mouse.
OS Mus sp.
PN WO9811225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI (DZIE/) DZIELEWSKA H E.
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Meada M, Nash A, Nicola NA, Rakar S, Willson T,
PI Zhang J.
DR WPI: 98-260970/23.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PS Claim 6: Page 90-92: 182pp; English.
CC The haemopoietin receptor (HR) NR6.3 is a form of the novel HR NR6.
CC Interaction between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and its
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SQ Sequence 938 BP; 243 A; 245 C; 272 G; 178 T;

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Query Match 18.2%; Score 304; DB 1; Length 938;
Best Local Similarity 100.0%; Pred. No. 1.6e-54;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1043 gacacgcttactctgctcagtgctgtgacacattcggagtcataagtggtgaaag 1102
Db 1 GGCACCTTACTTCTGTCAGATGCGTTGTAACCATTCGGGATCTATGGGTGAGAAAG 60

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Db 1399 GAGACGGCAGCATCTGCTGCTGCTCTGCTATGTTGCT 1440

RESULT 15

ID V70897 standard; cDNA; 259 BP.

AC V70897; (first entry)

DE Expressed sequence tag used to identify human Zcytor5.

KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1; cardiac pathology; heart enlargement; Zcytor5 ligand; EST; ss.

OS Unidentified.

PN W09849307-A1.

PD 05-NOV-1998.

PF 01-MAY-1998; U08865.

PR 13-FEB-1998; US-074721.

PR 01-MAY-1997; US-045287.

PR 01-MAY-1997; US-850030.

PR 13-FEB-1998; US-023890.

PA (ZYMO) ZYMOGENETICS INC.

PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,

PI Lok S, Presnell SR, Whitmore TE;

DR WPI; 99-034662/03.

PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.

PT down-regulating Zcytor5 natural ligands or detecting cardiostrophin-1

PT in blood

PS Example 1; Page 77; 55pp; English.

CC The present sequence represents an expressed sequence tag (EST)

CC used to identify cDNA encoding a protein designated Zcytor5, which is

CC a cytokinin-like receptor. Soluble Zcytor5 may be administered to

CC down-regulate the effects of a growth and/or maintenance factor in

CC thyroid, heart, and skeletal muscle for example to lessen the effect

CC of cardiostrophin-1 on cardiac pathologies, so preventing heart

CC enlargement. Zcytor5 could be used to detect cardiostrophin-1 in the

CC blood, and to discover other possible Zcytor5 ligands. A probe

CC comprising Zcytor5 DNA or RNA can be used to determine the presence

CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the

CC anti-idiotypic antibody could be used to purify Zcytor5 and

CC therapeutically to modify Zcytor5 ligand effects.

CC Sequence 259 BP; 53 A; 64 C; 81 G; 46 T;

Query Match 10.7%; Score 178.8; DB 1; Length 259;

Best Local Similarity 81.3%; Pred. No. 9,7e-29;

Matches 209; Conservative 0; Mismatches 47; Indels 1; Gaps 1;

QY 924 aggaattctcttcctcaagccaagatccagatccgctacgctgagagacagcgtagact 983

Db 1 AGGATTTCCTCTTCAAGCCAAATACAGATCCGCTANCGATGAGAGANAGTGTGANT 60

QY 984 ggaagtgtgtgagatgacgtcagcaaccacacccctcgtcgcgagccgagcccg 1043

Db 61 GGAAGGTGTGTGANGATGAGCAACCAACGACTTGTGCG-CTGNGCGGCTGAACCCG 119

QY 1044 gcaaccgttctacgtccaaagtgtgtgttaaccatcggagatctatgtgtcgaagaag 1103

Db 120 GCANCGTGTACTTGTGCAAGTGTGCTGCAANCCCTTGTGATCTATGCTNCAAGAAAG 179

QY 1104 cgggaatctgagagcagtgagccacccacccgctgctccacccctcgaagttagcgcc 1163

Db 180 CCGGATCTGATGATGATGAGCCAGCCACAGCGGCTTCAANTCCCGCAGTAGCGNC 239

QY 1164 cgggcccgggcggcggg 1180

Db 240 NGGGCCCGGGNGNGGG 256

Search completed: September 28, 1999, 16:45:17

Job time: 7302 sec

RESULT 4
 US-08-267-803B
 Sequence 8, Application US/08267803B
 Patent No. 5834183
 GENERAL INFORMATION:
 APPLICANT: Orr, Harry T.
 APPLICANT: Rannum, Laura P.W.
 APPLICANT: Chung, Ming-Yi
 APPLICANT: Zoghbi, Huda Y.
 TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
 Patent No. 5834183

TITLE OF INVENTION: Type 1 and Method for Diagnosing
 NUMBER OF SEQUENCES: 85
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Muelling, Raasch, Gebhardt & Schwapp
 STREET: P.O. Box 561415
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 55458-1415
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/267,803B
 FILING DATE: 28-JUN-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: McCormack, Myra H.
 REGISTRATION NUMBER: 36,602
 REFERENCE/DOCKET NUMBER: 110,00030120
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-305-1217
 TELEFAX: 612-305-1228
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10660 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 936..3384
 7S-08-267-803B-8

	Query Match	2.6%	Score 44	DB 4	Length 10660
	Best Local Similarity	57.1%	Pred. No. 0.29		
	Matches 80	Conservative 0	Mismatches 60	Indels 0	Gaps 0
QY 1534	ttgtgtccacatgaatgagcgcacactctggatatacccccagctgtggtaagttgsgygtatcg	1593			
Db 10498	TTTGATTCAAAATTTGAAACAATAATGTTTAAATAAATGTCGTGTACACAGTCAAGTT	10557			
QY 1594	caggccccccacacatctctttaataataaagaagctgttcagcgtataaaaaaaaaa	1653			
Db 10558	TATGTTTCACGATATCTGCTACTAATTAATTAATACAGTGCACCAATTCGCAAAAAAAAAA	10617			

RESULT 5
US-08-284-941-1
; Sequence 1, Application US/08284941
; Patent No. 5863756

GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J
APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOLEY GODMARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,941
FILING DATE: 2 August 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NEEDLEY P.H.D., RICHARD L.
REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: CHIR-009/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 843-5070
TELEFAX: (415) 857-0663
TELEX: 380818 COOLEY PA
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4403 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 170..3077
US-08-284-941-1

Query Match	2.6%	Score 43.4	DB 4	Length 4403
Best Local Similarity	51.9%	Pred. No. 0.31		
Matches	98	Conservative	0	Mismatches 91
				Indels 0
				Gaps 0
QY	20	gcgcgcccaatgacgcgcgtgcgagaccgagaccccaatctgcaccccgagatcgccccg	79	
Db	146	GCGCCCGCGCAGACCTTCGCCCGTATGCTCTCGCGCGCGCGCTGCGCCCGGCCCGG	205	
QY	80	ccccatcacggcgttcagttcacgcgcgcgtttgcgcgcacccccaatgcgcgcgtgcgc	139	
Db	206	CG	265	
QY	140	ccgggcccgcgtgcaccaatcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	199	
Db	266	GCGGGGGCGCGCGCGCGCGCGCGGGTTCGGGCGCGCGCGCGCGCGCGCGCGCGCG	325	
QY	200	ccctcgtttg	208	
Db	326	CTGCTGCTG	334	


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RESULT      6
US-08-738-349-1
; Sequence 1, Application US/08738349
; Patent No. 5869638
; GENERAL INFORMATION:
; APPLICANT: Takeshita, Sunao
; APPLICANT: Okazaki, Makoto
; APPLICANT: Kawai, Shinji
; APPLICANT: Tsujimura, Atsushi
; APPLICANT: Amann, Egon
; TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
; TITLE OF INVENTION: Process for its Production
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/738,349
; FILING DATE: 25-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/364,439
; FILING DATE:
; APPLICATION NUMBER: US 08/112,061
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Barker, M. P.
; REGISTRATION NUMBER: 32,013
; REFERENCE/DOCKET NUMBER: 02481.1323-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3581 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; STRAIN: osteoblastic cell line MC3T3E1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 284..2671
; US-08-738-349-1

Query Match          2.6%; Score 43.4; DB 4; Length 3581;
Best Local Similarity 76.8%; Pred. No. 0.3;
Matches    53; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY   1605 aacatctcttaataataagagcgttgcaggtaaaaaa
Db   3469 AAGCACTTTGAAATATAAAAAAAGATTCTTTTTTA
QY   1665 aaaaaaaaaa 1673
Db   3529 AAAAAAAAAA 3537

RESULT      7

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PCT-US93-02147A-1
Sequence 1, Application PC/TUS9302147A
GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J
APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PAGE 4 AND
TITLE OF INVENTION: PAGE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02147A
FILING DATE: 19930309
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,629
FILING DATE: 09-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH.D., RICHARD L
REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: CHIR-009/00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-7622
TELEFAX: (415) 857-0663
TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4403 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (cDNA)
FEATURE:
NAME/KEY: CDS
LOCATION: 170..3077.
PCT-US93-02147A-1

Query Match 2.68; Score 43.4; DB 5; Length 4403;
Best Local Similarity 51.9%; Pred. No. 0.31;
Matches 98; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

OY 20 ggcgccatgacgcgcgtgacgacccgcgcgcaccccaatctgcacccgcgcgaatcgccccc 79
    |||||
Db 146 ggcgcgcgcgcgcgcgtgacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 205
    |||||

OY 80 ccccatcgcgcgcgttgcacgtacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 139
    |||||
Db 206 cgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 265
    |||||

OY 140 ccggagcccgctgcgcacacacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 199
    |||||
Db 266 gcggggggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 325
    |||||

OY 200 cctctgttg 208
    |||||
Db 326 CTGCTGCTG 334

RESULT 8
PCT-US94-03705-3
Sequence 3, Application PC/TUS9403705
GENERAL INFORMATION:

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Query Match      2.68; Score 43.4; DB 5; Length 2745;
Best Local Similarity 62.48; Pred. No. 0.28;
Matches 68; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

OY      102  cgcgcgctgcgcgcaccccccaatgcgccgcggtgcgccgggcccgcgtgcaccaatcgc 161
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       795  CACGCCCTGTTGGCGCTCTCGGCAGTGGCGGGGGCGCGCCCTCCACCATCGCCGCCCTCCG 854
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      162  cgcgcgcgcgcgcgcgcgcgcgtgccgcgtgtggtgtgcctctgttgc 210
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       855  GGCTGCGGCTGCTGCGCTGCGCTGCTACCGGCTGCTGTGGCTACTGCTGTCT 903
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT      9
US-08-242-677-1
; Sequence 1, Application US/08242677
; Patent No. 5677143
; GENERAL INFORMATION:
; APPLICANT: GAYNOT, Richard B
; APPLICANT: Wu, Foon W.
; TITLE OF INVENTION: Cellular Nucleic Acid Binding Protein
; TITLE OF INVENTION: and uses thereof in regulating Gene Expression and in the
; TITLE OF INVENTION: Treatment of AIDS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX

```

```

Query Match: 2.6%; Score 43.2; DB 2; Length 5173;
Best Local Similarity 79.7%; Pred. No. 0.36;
Matches 51; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1610 tcctctaataataatcaagaggtgttcaggttaaaaaaaaaaaaaaaaaa 1669
    | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5073 TTTAATAAATATTTTAAAGCAATGTCCATAAAAAAAAAAAAAAAAAAA 5132
    | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1670 aaaa 1673
    ||||
Db 5133 AAAA 5136

```

RESULT 10 RESULT
US-08-467-607-2
Sequence 2, Application US/08467607
Patent No. 5783434
GENERAL INFORMATION:
APPLICANT: TUNG, JAY S.
APPLICANT: SINHA, SUKANTO
APPLICANT: MCCONLOGUE, LISA
APPLICANT: TATSURO, GREN
APPLICANT: ANDERSON, JOHN
APPLICANT: CHRYSLER, SUSANNA
TITLE OF INVENTION: NOVEL CARBESIN AND METHODS AND
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATHENA NEUROSCIENCES
STREET: 800 F. Gateway Blvd.
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,607
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DUVAL, JEAN M.
REGISTRATION NUMBER: 32,731
REFERENCE/DOCKET NUMBER: 002010-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
TELEFAX: (415) 877-8370
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1558 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 103..1011
US-08-467-607-2

Query Match 2.6%; Score 43; DB 3; Length 1558;
Best Local Similarity 49.6%; Pred. No. 0.29;
Matches 67; Conservative 13; Mismatches 55; Indels 0; Gaps 0;

QY 1539 tccacatggtgacacttgatatacccccagtggtgtaagggttggtatgcagg 1598
DB 1373 TCMCATCTTATTTCACCTTAGRATCMAGGCTGGRGRRGRCAGGCAATTGTCA 1432
QY 1599 cctcccaaatctcttaataataaaggaggtgtcaggttaaaaaaaaaaaaaa 1658
DB 1433 TCCCCMTCCCCCGANTGNTGRAMAARAAATCTGCCCTCCCGAAAAAAAAAA 1492
QY 1659 aaaaaaaaaaaaaa 1673
DB 1493 AAAAAAAAAAAAAA 1507

RESULT 11
US-08-469-362-2
Sequence 2, Application US/08469362
Patent No. 5849711
GENERAL INFORMATION:
APPLICANT: TUNG, JAY S.
APPLICANT: SINHA, SUKANTO
APPLICANT: MCCONLOGUE, LISA
APPLICANT: SEMKO, CHRISTOPHER M.F.
TITLE OF INVENTION: NOVEL CATHEPSIN AND METHODS AND
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATHENA NEUROSCIENCES
STREET: 800 F. Gateway Blvd.
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,362
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DUVAL, JEAN M.
REGISTRATION NUMBER: 32,731
REFERENCE/DOCKET NUMBER: 002010-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
TELEFAX: (415) 877-8370
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 1558 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 103..1011
US-08-469-362-2

Query Match 2.6%; Score 43; DB 4; Length 1558;
Best Local Similarity 49.6%; Pred. No. 0.29;
Matches 67; Conservative 13; Mismatches 55; Indels 0; Gaps 0;

QY 1539 tccacatggtgacacttgatatacccccagtggtgtaagggttggtatgcagg 1598
DB 1373 TCMCATCTTATTTCACCTTAGRATCMAGGCTGGRGRRGRCAGGCAATTGTCA 1432
QY 1599 cctcccaaatctcttaataataaaggaggtgtcaggttaaaaaaaaaaaaaa 1658
DB 1433 TCCCCMTCCCCCGANTGNTGRAMAARAAATCTGCCCTCCCGAAAAAAAAAA 1492
QY 1659 aaaaaaaaaaaaaa 1673
DB 1493 AAAAAAAAAAAAAA 1507

RESULT 12
US-08-850-392-2
Sequence 2, Application US/08850392
Patent No. 5858982
GENERAL INFORMATION:
APPLICANT: TUNG, JAY S.
APPLICANT: SINHA, SUKANTO
APPLICANT: MCCONLOGUE, LISA
APPLICANT: SEMKO, CHRISTOPHER M.F.
TITLE OF INVENTION: NOVEL CATHEPSIN AND METHODS AND
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATHENA NEUROSCIENCES
STREET: 800 F. Gateway Blvd.
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,392
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,362
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: DUVAL, JEAN M.
REGISTRATION NUMBER: 32,731
REFERENCE/DOCKET NUMBER: 002010-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
TELEFAX: (415) 877-8370
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1558 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:

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; ORGANISM: Trichoderma reesei
; STRAIN: QM9414
US-08-911-020-3

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FEATURES
LOCATION/QUALITIES
1. 466
SOURCE
/organism="Homo sapiens"

Eutheria; Primates; Catarrhini; Hominoidea; Homo.

RESULT 7
 A1185924
 LOCUS
 DEFINITION
 A1185924 477 bp mRNA EST 29-OCT-1998
 g950c003.x1 Soates.-fetal_lung_NBHL19W Homo sapiens cDNA clone
 IMAGE:1142408 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR ;
 mRNA sequence.
 ACCESSION A1185924
 NID 93736562
 VERSION A1185924.1 GI:3736562
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 477)
 NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 On Feb 17, 1998 this sequence version replaced gi:2150926.

FEATURES	Location/Qualifiers
source	1. .477

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1742408"
/clone.lib="Soares.fetal_lung_NbHL9W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Lung; Vector: pRT3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
15'-GTGACCAATCTGAACTGGAGCGCGCGCAATTTTTTTTTTTT-3'}
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library. Soares
fetal heart NbHL9W."

```

Query Match	21.78;	Score 362.8;	DB 43;	Length 477;
Best Local Similarity	85.68;	Pred. No. 3.7e-60;		
Matches 403; Conservative	0;	Mismatches 68;	Indels 0;	Gaps 0

[illegible]

Db	187	CGTCCCCCGAGAGTCTCCGGGTACTCAACGCGTCCACCTTGCGTCTGGCCCTGGCCAA	246
QY	439	ccttaatgggttccaagcagcagcagtcagagagacaactgtgtgtgtcaagcccgagacgagc	498
Db	247	CGTAAATGGGTCCAGGAGAGGGTCCGGGGACAACCTCGGTGTCCACGCGCGGTGACGCAG	306
QY	499	catctgtgcgcgtacctgtcctcatgtgtgtgtgtgcccccttgaaagccgcttaacatag	558
Db	307	CATCGTGGTGTGCTCGGCTGTATTTTGGCTTGCCGCCAGAGAAACCGTCAACATGAG	366
QY	559	ctgtctgtgtcccggaacatgaagatctcaagtgcgcgttgacaccggtgtgacacggyga	618
Db	367	CTGTGCTGCCAATAAATGAAGACTTGACCTGCGCGTGAGAGCCAGGGGGCCACGCGNGA	426
QY	619	gaacatttcatcaccaactactccttccttaagtaacaagttgagttgtgtcgg	669
Db	427	GACCTTCCTCCACCACTACTCTCCTCAAGTACAACTTAAAGTGTATGG	477

RESULT	8
AI394468	
LOCUS	AI394468
DEFINITION	tff7d12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105495 3'
ACCESSION	AI394468
NID	94224015
VERSION	AI394468.1 GI:4224015
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (cases 1 to 462)
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/STGAP), Tumor Gene Index
Unpublished (1998)
On Feb 17, 1998 this sequence version replaced q1:2887603.

Contact: Robert Strausberg, Ph.D.
 Tel.: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution Information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbdp/image/image.html
 Insert Length: 1631 Std Error: 0.00
 Seq Primer: -400P From Gbco
 High quality sequence stop: 454.
 Location/Qualifiers
 1. 462

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="10: 1"
/clone="IMAGE:2105495"
/clone_1lb="NC1_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pRTT3-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5']
TGTTCACCAATCTGAAGTGGAGCGGCCCATATCTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pRTT3 vector.
Library is normalized, and was constructed by Bento

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/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; This library
consists of a mixture of individually tagged normalized
libraries constructed from rat placenta, adult lung,
brain, liver, kidney, heart, spleen, ovary, and muscle.
The tag is a string of 3-5 nucleotides present between the
Not I site and the oligo-dr track which allows
identification of the library of origin of a clone within
the mixture."

BASE COUNT 87 a 134 c 120 g 87 t
ORIGIN

Query Match 23.4%; Score 391.8; DB 45; Length 428;
Best Local Similarity 94.8%; Pred. No. 1.1e-65;
Matches 405; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 660 ggtgtacggtcagataacacatgtgaggagataccacactgtggccctcactcattcc 719
DB 2 GGCCCTCAATCAGACACACATGTGAGATATCACACTGTGGCCCTCAGTGTGCC 61
QY 720 atatacccaaggacctgtgcccccttcactccctatgagatctgggtgtgaagccaccatc 779
DB 62 ATATCCCAAGACCTGGCCCTCTTCACGCCCTATGAGATCTGGGGAAGCCACCAATC 121
QY 780 gcttagcctcagacagatctgtctccacactgagctcctcgtgagctgtgaccacg 839
DB 122 GCTGTGCTTACCGAGATGTGACGTGCTACACTGATCTCTGACGCGTGACACAG 181
QY 840 acccccacacacgctgtcagctgtgagccgctgtggggcttgaggagacacacgtgtgtc 899
DB 182 ACCCTCCACCGACGCGACGAGCGGCGGTGGGGGCTGGAGGACGAGTGTGCTC 241
QY 900 gctgtgtctcaccacacagctctcaagatctcctctccaaagcaagctcagatccgt 959
DB 242 GCTGGGTCTCACCACGACGCTCAGAGATTCTCTCCAAAGCAATACAGATTGCT 301
QY 960 accgctgtgagagacagcctgtgagctgtgagctgtgagctgtgagctgtgagctgt 1019
DB 302 ACCGCTGTGAGACAGCGGTGAGCTGTGAGGTGTGATGCTGACACACGACCTCTCT 361
QY 1020 gccgtctcgcgcgcctgaaagccgcgcgccttactctgtccaaagctgtgttaacat 1079
DB 362 GCCGTCTCCGGGCTTGAACCCGCGACCTTACTTCGTCGAAGTTCGTGTAAACCAT 421
QY 1080 tcgggat 1086
DB 422 TCGGAT 428

RESULT 6
AI421423 474 bp mRNA EST 30-MAR-1999
LOCUS ttf25h01.x1 NCI-CGAP Brn23 Homo sapiens cDNA IMAGE:2097265 3'
DEFINITION similar to SW.1166 MOUSE 000560 INTEREDWIN-6 RECEPTOR BETA CHAIN
PRECEDSOR: mRNA sequence.

ACCESSION AI421423
NID 94267354
VERSION AI421423.1 GI:4267354
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BrGAP), Tumor Gene Index

JOURNAL
COMMENT Unpublished (1998)
On Apr 7, 1998 this sequence version replaced gi:3034955.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldi, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bdrip/image/image.html

Insert Length: 1664 Std Error: 0.00
Seq primer: -400P from Glibco
High quality sequence stop: 450.
Location/Qualifiers
1. 474

FEATURES

SOURCE

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2097265"
/clone_id="NCI-CGAP_Brn23"
/tissue_type="gliblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dr) primer (5'
TGTACCAATCTGAGTGGGCGCGCCGACATCTTTTGTGTGTGTGTGTGTGTGT
T 3'); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldi."

BASE COUNT 81 a 181 c 128 g 83 t 1 others
ORIGIN

Query Match 21.8%; Score 364.2; DB 46; Length 474;
Best Local Similarity 85.4%; Pred. No. 2e-60;
Matches 405; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 196 gtcgctctgttgcctctgtctgtctgtctgtctgtctgtctgtctgtctgtctgt 255
DB 1 GCCCTGCTGCTGCTCTGTGCTCTGTGCTCTGTGCTCTGTGCTCTGTGCTCTGTGCT 60
QY 256 tttatcagccccagagacacacacctctcattcagctcctccctcgaagctacgtctc 315
DB 61 TGTGATCACTCCCAAGATCCCAAGATCCCAAGATCCCAAGATCCCAAGATCCCAAG 120
QY 316 tatatacagagac 375
DB 121 AGTGCAGGAGACCCACGAGACGAGACCCGAGGAGGCTCTTACTGAGACCTCAATGG 180
QY 376 cgcgcgcgcctctgagctgtccgcctccttaaacctcacaacctgtgacctgtgc 435
DB 181 CCGCTGCCCCCTGAGACTCTCCGCTACTCAACGCGCTCCACCTTGCTTGCCCTGCG 240
QY 436 taacctaatggtctcagagcagcagcagcagcagcagcagcagcagcagcagcagc 495
DB 241 CAACCTCAATGAGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
QY 496 cagcattctgctgtctcctcctctatgttgcctgtgccccctgagagagcctttaacat 555
DB 301 CACATCTCTGCTGCTGCTCTCTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 556 cagctgtgtgtcccgaaatgaaagatctacgtgcgcgtgtgacacacgggtgcaacgg 615
DB 361 CACTGCTGTGTCAGAAACATGAAAGACTTGACTGCGCTGTGAGCGCCAGGGGCCACGG 420
QY 616 gaggacattcttatatacaacacacacacacacacacacacacacacacacacacac 669
DB 421 NGAGACCTTCTCCACACCAACTCTCCCAAGTACAAAGTACAAAGTACAAAGTACAA 474

QY 1536 tgggtccacatgatggtcacttgat 1562
 Db 27 TGGTCCACATGATGCTCACATTGGAT 1
 RESULT 4
 LOCUS AA039053 445 bp mRNA EST 29-AUG-1996
 DEFINITION m19907.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
 clone IMAGE:474733 5', mRNA sequence.
 ACCESSION AA039053
 NID 51514788
 VERSION AA039053.1 GI:1514788
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 445)
 Authors: Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Giesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 TITLE
 JOURNAL
 COMMENT
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:263477
 Seq primer: -28M13 rev2 from Amer sham
 High quality sequence stop: 441.
 Location/Qualifiers
 1..445
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_image="IMAGE:474733"
 /clone_lib="Soares mouse embryo NbME13.5 14.5"
 /sex="unknown"
 /tissue_type="embryo"
 /dev_stage="13.5-14.5dpc total fetus"
 /lab_host="DH10B"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5'
 TGTTCACATCTGAGATGGAGCGCCGCGGAATTTTCTTTTCTTTTCTTTT
 T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
 State Univ., from 2]; double-stranded cDNA was ligated to
 Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of the modified
 pT7T3 vector. Library went through one round of
 normalization, and was constructed by Bento Soares and
 M. Fatima Bonaldo.
 BASE COUNT 85 a 129 c 124 g 107 t
 ORIGIN
 Query Match 25.7%; Score 430.6; DB 27; Length 445;
 Best Local Similarity 98.0%; Pred. No. 4.3e-73;
 Matches 436; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1207 cagctcgggcccggcgccgagctcaagcagctcccgctgctcaagaagcagc 1266
 Db 445 CAGCTCGGCGCCGGTGGCGGAGCTCAAGCAGTCTCGCTGCTCAAGAGCAGCG 386

QY 1267 atactctgaaccttagttccgctctgaacacagtggtgcttgatgcagaagtc 1326
 Db 385 ATACTGCTCGAACCTTAGTTCCGCTGTACGACAGTGGCGTCTTGATGACGAATG 326
 QY 1327 acacaagaccggaacacagagcagagggatccgctctgggacacgggagggcag 1386
 Db 325 ACACAAGACCCGAACACAGACAGAGGGGATCCCTCGGGCAGACGGGGCGAG 266
 QY 1387 aggtctccggttaacttaagataagagccatccctctgctggttcagacctgagagc 1446
 Db 265 AGGTCTCGCGGCTAAACTTAAGATAGGACATCTCTGCTGGGTGACACTGAGAGC 206
 QY 1447 tcacctgaattggaagccctctgtaccatctgggcaacaagaacctacagagctgg 1506
 Db 205 TCACCTGAATTGGAGCCCTCTGTACATCTGGCCAAAGAAACCTACAGAGGCTGG 146
 QY 1507 ggcacatagctccacacacacacacagcttggttcacatgagtgacactggtatcac 1566
 Db 145 GGCACATAGCTCCACCAACACACACACTTTGGTCCACATGATGTGACACTTGATATAC 86
 QY 1567 ccagtggtgtaaggttggggatgtatgcagggcctccacacatcctttaataataa 1626
 Db 85 CCCAGTGTGGGTAGGGTGGGATGTGACAGGGCCTCCCAAGAGTCTCTTAATAATAA 26
 QY 1627 aggaagtgttcaggttaaaaaaa 1651
 Db 25 AGGAGTTGTTCAGGTCCGAAAAA 1
 RESULT 5
 LOCUS AA866388
 DEFINITION
 AA866388 428 bp mRNA EST 05-FEB-1999
 UI-R-A0-aj-f-04-0-UI-s3 UI-R-A0 Rattus norvegicus cDNA clone
 UI-R-A0-aj-f-04-0-UI-3, similar to gb|AC003112|AC003112 Human DNA
 from chromosome 19 specific cosmid R30292, genomic sequence,
 complete sequence [homo sapiens], mRNA sequence.
 ACCESSION AA866388
 NID 94230568
 VERSION AA866388.1 GI:4230568
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE 1 (bases 1 to 428)
 Authors: Bonaldo, M.F., Lennon, G. and Soares, M.B.
 Title: Normalization and subtraction: two approaches to facilitate gene
 discovery
 Journal Genome Res. 6 (9), 791-806 (1996)
 Medline 97044477
 Comment On Mar 16, 1998 this sequence version replaced gi:2961849.
 FEATURES
 MEDLINE
 COMMENT
 Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: mesores@iue.wesg.uiowa.edu
 Oligo-dT track not found, Not I site shown in beginning of sequence
 is likely internal to the message. cDNA library preparation: M.
 Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
 through Research Genetics
 Seq primer: M13 Forward.
 Location/Qualifiers
 1..428
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /map="between D1S1765 and Uga"
 /clone="UI-R-A0-aj-f-04-0-UI"
 /clone_lib="UI-R-A0"

14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 96 a 138 c 147 g 101 t

Query Match 27.4%; Score 457.8; DB 26; Length 482;
Best Local Similarity 99.4%; Pred. No. 2.8e-78;
Matches 470; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 665 tacgtcagatatacatatgtgagaggtacacacgtggccctcactcatcgcatac 724
|||||
DB 482 TAGGCTAGGATTAACATATGAGAGTACCACACTGGGCTTCATGCTATTC 423
QY 725 cccaagacctggccctctcactcctatgagatctgggtggaagccacaatcgcta 784
|||||
DB 422 CCCAGACCTGGGCTCTTCTACTCCCTATGAGATCTGGGAGGAGCCCAATTCGCTA 363
QY 785 ggtcagcaagatctgttctcacaactgagatctcctgagcgtgtgacacagaccc 844
|||||
DB 362 GGGCTACCAAGATCTGATGCTCTCACACTGATGCTCTGACGCGGTGACACGACGCC 303
QY 845 ccaccagctgcaagctgagacgagctgggggagctggagagacagcagctgagctg 904
|||||
DB 302 CCACCCACATGTCAGCTGAGCCGCTTGGGGCTTGGAGACAGCTGAGTGTGGCTGG 243
QY 905 gtctcaccacagctctcacaagattcctcttccaaagccaaagtcag-ctccgctacg 963
|||||
DB 242 GTCTACACACAGCTCTCAAGATTCCTCTTCCAAAGCAAGTACAGTATTCGCTACG 183
QY 964 cgtgagagacagcgtgagctggaagtggtgagatgacgtcaagcaacagacccctcgcg 1023
|||||
DB 182 CGTGAGAGACAGCTGAGCTGAGAGGTGGATGAGAGTACAGCAACAGCACTCTCTCCG 123
QY 1024 tctcgagcctgagacgagcagcagcttcttctcctcagagtggtgtgataccatcgg 1083
|||||
DB 122 TCTGCGGGCTGAGGCCGCGACCGCTTCTTCTGCTCAAGTGCTGTAACTCCATTCGG 63
QY 1084 gatctacggtcgaagagcggaatcctgagcagtgagtgagccacccacgg 1136
|||||
DB 62 GATATAGGCTCGAAGGCGGGAATCTGAGCGAGTGAAGCCACCCCATTCG 10

RESULT 3
AA049278 503 bp mRNA EST 30-DEC-1996
LOCUS AA049278/c
DEFINITION mj45c04.r1 Soares mouse embryo NbMEL3.5 14.5 Mus musculus cDNA
clone IMAGE:479046 5', mRNA sequence.

ACCESSION
NID AA049278
VERSION 91755309
KEYWORDS AA049278.1 GI:1755309
SOURCE EST
ORGANISM house mouse.
Mus musculus

REFERENCE
AUTHORS Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 503)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Giesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenger, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theisinger, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Materston, R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT On Dec 30, 1996 this sequence version replaced gi:1528949.

Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:289790
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 486.

FEATURES
source location/Qualifiers

1..503
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="479046"
/clone_lib="Soares mouse embryo NbMEL3.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="Vector: pRTT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAGTGGAGCGGCGGGAATTTTCTTTTCTTTTCTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pRTT3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M. Fatima Bonaldo."

BASE COUNT 85 a 158 c 154 g 106 t

Query Match 26.9%; Score 449.4; DB 29; Length 503;
Best Local Similarity 98.0%; Pred. No. 1.1e-76;
Matches 497; Conservative 0; Mismatches 6; Indels 4; Gaps 4;

QY 1056 tctgcaagtgctgttaaccatctggagatctatggtcgaagagcggaatctgga 1115
|||||
DB 503 TCGTCAAGTGGCTGTGAACCATTCGGGATCTATGGGTGGAAGAGCGGGAATCTGGA 444
QY 1116 gctgagtgagacccacccacgctgctcaccctcgaagtgagccgagccggcg 1175
|||||
DB 443 GCGAGT-GAGCCACCCACCGCTGCTCCACCCCTCGAATGA-TGCCCGGGCCGGCGC 386
QY 1176 gctgagtgagacccgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcga 1235
|||||
DB 385 GCGGGGTGTTC-CGAGCGCGGGGGCGGA-CCAGCTCGGGCGGGTGGCGGAGCTCA 328
QY 1236 agcagctcctcgtgctgctcaagaagcagcagctcgtcgaacctaagtttcgcgctgt 1295
|||||
DB 327 AGCAGTTCCTGGCTGGCTGCAAGAGACGACATCTCTGAACTTAGTTCCGCTGT 268
QY 1296 acgacagtgctgctgtgagatgcagagatcacacaagaccggaagcagagagagga 1355
|||||
DB 267 ACACACAGTGGCTGCTTGGATCGAGAGTCAACACAGACCCGAAACAGAGAGAGGGA 208
QY 1356 tctgctcctggcagacagcgagtgctgagagagtgctgctgctgctgctgctgctgctg 1415
|||||
DB 207 TCTGCTCCTGGCGAGAGGGGGTGGCGGAGAGTCTCTCGGCTTAACCTTAAGGATAG 148
QY 1416 gcatcctcctgctgctgctgagacctgagagctacacgtgaattgagccctcgtacacat 1475
|||||
DB 147 GCATCCTCTGCTGGGTGAGACTGAGAGCTCACTGGAATTTGAGAGCCCTCTGTACAT 88
QY 1476 ctgggcaacaagaacatccagagagctgggagacaaatgagctccacaacacagcct 1535
|||||
DB 87 CTGGGCAACAAAGAACTACAGAGGCTGGGCAACATGAGCTCCACACACACACTT 28

VERSION MA049280.1 GI:1755311
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 464)
 Maier, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT On Dec 30, 1996 this sequence version replaced gi:1528951.
 Contact: Maier, M./Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:289787
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 437.
 Location/Qualifiers
 1..464
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:479043"
 /clone_1lb="Soares mouse embryo NbME13.5 14.5"
 /sex="unknown"
 /tissue_type="embryo"
 /dev_stage="13.5-14.5dpc total fetus"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - 01190(dT) primer [5',
 TGTTCACATCTGAGTGGAGCGCGCCGCGAATTTTATTTTATTTT
 T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
 State Univ., from 2]; double-stranded cDNA was ligated to
 Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of the modified
 pT73 vector. Library went through one round of
 normalization, and was constructed by Bento Soares and
 M. Fatima Bonaldo."

BASE COUNT 102 a 144 c 130 g 88 t

Query Match 27.7%; Score 464; DB 29; Length 464;
 Best Local Similarity 100.0%; Pred No. 1.9e-79;
 Matches 464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 558 gctcgtggtccgcggaacatgaagatctcagtcgctgcgacacgggtgacacaggg 617
 |||||||
 Db 1 gctcgtggtccgcggaacatgaagatctcagtcgctgcgacacgggtgacacaggg 60
 |||||||
 QY 618 aggcattcttaccatacctaactctccctcaagtaagaagctgaggtgtaagtcagata 677
 |||||||
 Db 61 agacattcttaccatacctaactctccctcaagtaagaagctgaggtgtaagtcagata 120
 |||||||
 QY 678 acacatgtgaggaatcacacacgttgaggcctcactatccatcccccaaggaactgg 737
 |||||||
 Db 121 acacatgtgaggaatcacacacgttgaggcctcactatccatcccccaaggaactgg 180
 |||||||
 QY 738 ccctcttactccctatgagatctgggtggaagccaccaatcgcttaggtcagaagat 797
 |||||||

Db 181 cccctttacacctcctatgagatctgggtgagaccaccacaaatgcccttagcgcacgaagat 240
 QY 798 ctgattcttcacacatgattctcctgagcctggtgacacaggaaccccccacagctgc 857
 |||||||
 Db 241 ctgattcttcacacatgattctcctgagcctggtgacacaggaaccccccacagctgc 300
 |||||||
 QY 858 acgtgagccggttggggggtcctggaagacacagctgagctggtggtctcaccacag 917
 |||||||
 Db 301 acgtgagccggttggggggtcctggaagacacagctgagctggtggtctcaccacag 360
 |||||||
 QY 918 ctcccaaggaattctcttcacagacgaatcacacacgctcgcctggtggaagacgg 977
 |||||||
 Db 361 ctcccaaggaattctcttcacagacgaatcacacacgctcgcctggtggaagacgg 420
 |||||||
 QY 978 tggactggaagtggtgattgacgtcagcaacacagactctgc 1021
 |||||||
 Db 421 tggactggaagtggtgattgacgtcagcaacacagactctctgc 464
 |||||||

RESULT 2
 LOCUS W66776/c 482 bp mRNA EST 14-JUN-1996
 DEFINITION me17b11.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
 clone IMAGE:387741 5' similar to PIR:B38252 B38252 granulocyte
 colony-stimulating factor receptor precursor ; mRNA sequence.
 W66776
 91378694
 W66776.1 GI:1755694
 EST.
 VERSION W66776.1
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 482)
 Maier, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT On Apr 14, 1993 this sequence version replaced gi:1785250.

CONTACT: Maier, M./Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:239573
 Possible reversed clone: similarity on wrong strand
 Seq primer: E7primer
 High quality sequence stop: 359.
 Location/Qualifiers
 1..482
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /map="10 pter-ten"
 /clone="IMAGE:387741"
 /clone_1lb="Soares mouse embryo NbME13.5 14.5"
 /sex="unknown"
 /tissue_type="embryo"
 /dev_stage="13.5-14.5dpc total fetus"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - 01190(dT) primer [5',
 TGTTCACATCTGAGTGGAGCGCGCCGCGAATTTTATTTTATTTT
 T 3'], on equal amounts of mRNA from 2 13.5dpc and 2

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 28, 1999, 15:38:03 ; Search time 2095.87 Seconds

(without alignments)
1574.548 Million cell updates/sec

Title: US-09-037-657-14

Perfect score: 1673
Sequence: 1 ggcacgagctcgtctcgtcgcg.....aaaaaaaaaaaaaaaaaaaaa 1673

Scoring table: IDENTITY_NUC

Searched: 2546578 seqs, 986266752 residues

Database :

EST:
1: em_est1.*
2: em_est2.*
3: em_est3.*
4: em_est4.*
5: em_est5.*
6: em_est6.*
7: em_est7.*
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9: em_est9.*
10: em_est10.*
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12: em_est12.*
13: em_est13.*
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18: em_est18.*
19: em_est19.*
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24: gb_est5.*
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33: gb_est14.*
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35: gb_est16.*
36: gb_est17.*
37: gb_est18.*
38: gb_est19.*
39: gb_est20.*
40: gb_est21.*
41: gb_est22.*
42: gb_est23.*
43: gb_est24.*
44: gb_est25.*
45: gb_est26.*
46: gb_est27.*
47: gb_est28.*
48: gb_est29.*
49: gb_est30.*
50: gb_est31.*
51: gb_est32.*
52: em_est20.*
53: em_est21.*

54: em_est22.*
55: em_est23.*
56: em_est24.*
57: em_est25.*
58: em_est26.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query length	DB ID	Description
1	464	27.7	464	29	AA049280 m45602.r
2	457.8	27.4	482	26	W66776 me17b1.r1
3	449.4	26.9	503	29	AA049278 m45604.r
4	430.6	25.7	445	27	AA039053 m19407.r
5	391.8	23.4	428	45	AA866388 m19407.r
6	364.2	21.8	474	46	AA821423 lf2501.x
7	362.8	21.7	477	43	AA185924 qe50c05.x
8	355.4	21.2	462	45	AA1394468 lf79d12.x
9	354	21.2	466	43	AA1161002 qb69g04.x
10	354	21.2	466	43	AA1185780 ge44h04.x
11	343.4	20.5	390	26	W17583 mb75b01.r1
12	334	20.0	447	43	AA187074 qe38a03.s
13	324.2	19.4	431	45	AA1333812 qp93e12.x
14	323.4	19.3	470	43	AA1233311 EST229999
15	318.8	18.6	444	41	AA1071408 m19407.r
16	311.4	18.6	417	44	AA1269388 q126b05.x
17	296.8	17.7	332	48	AA1579568 m19407.r
18	284.4	17.0	339	48	AA1574687 m19407.r
19	284.2	17.0	385	50	AA1670108 we65f03.x
20	246.4	14.7	410	27	AA042914 zK56f01.s
21	215.6	12.9	262	50	AA032198 AV032198
22	204.8	12.2	227	30	AA270365 wa63h12.r
23	202	12.1	225	48	AA1575060 m19407.r
24	195.2	11.7	438	27	AA043001 zK56f01.r
25	191.2	11.4	465	26	W46604 zc32h10.s1
26	185.8	11.1	273	23	R87407 ym88d09.s1
27	172	10.3	229	49	AA010798 AV010798
28	149.4	8.9	167	49	AA011309 AV011309
29	148.8	8.9	144	42	AA1074921 oy04d08.s
30	143.6	8.6	455	46	AA925924 m19407.r
31	131.8	7.9	247	32	AA377893 EST90550
32	131.8	7.9	218	22	AA14009 EST00035 Ch
33	129.8	7.8	237	25	N78873 zb17h05.s1
34	109.8	6.6	234	47	AA1535068 m19407.r
35	105.6	6.3	469	40	AA922128 OM45e12.s
36	85.8	5.1	467	29	AA127694 zK89e11.r
37	71.4	4.3	394	40	AA927378 om27a08.s
38	62	4.3	431	28	AA121532 zK89e11.s
39	56.8	3.4	1138	45	AA1374006 SMOVAFAP
40	56.6	3.4	107	27	AA014965 mb23e02.r
41	56.2	3.4	398	44	AA1264328 q109c05.x
42	56.2	3.4	389	46	AA1417616 t980c02.x
43	52.4	3.1	641	45	AA157868 qv13b02.x
44	51.6	3.1	1056	26	W42205 mc69e09.r1
45	50.6	3.0	729	39	AA849564 EST192331

ALIGNMENTS

RESULT 1
AA049280 464 bp mRNA
LOCUS m45602.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA
DEFINITION clone IMAGE:479043 5' similar to SW:116B MOUSE 000560 INTERLEUKIN-6
ACCESSION AA049280
NID g1735311
RECEPTOR BETA CHAIN PRECURSOR ; mRNA sequence.

REFERENCE
 1 (bases 1 to 464)
 AUTHORS
 Bernaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL
 Genome Res. 6 (9), 791-806 (1996)
 MEDLINE
 97044477
 COMMENT
 On Sep 12, 1996 this sequence version replaced gi:1404537.

Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 The sequence tag present in the cDNA between the NotI site and the
 oligo-dt track served to identify it as a clone from the normalized
 adult lung library. cDNA Library Preparation: M. Fatima Bernaldo,
 Ph.D. Clone distribution: clones will be available through Research
 Genetics

Seq primer: M3 Forward

FEATURES
 source

Location/Qualifiers
 1..464
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-C2-nb-d-08-0-UI"
 /clone_1lb="UI-R-C2"
 /dev_stage="adult"
 /lab_host="DHI0B (Life Technologies)"
 /note="Vector: p773D-pac (Pharmacia) with a modified
 polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-C2
 library is a subtracted library derived from the UI-R-C1
 library, which is a subtracted library derived from the
 UI-R-C0 library. The UI-R-C0 library consisted of a
 mixture of individually tagged normalized libraries
 constructed from rat placenta, adult lung, brain, liver,
 kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
 embryo. The tag is a string of 3-5 nucleotides present
 between the Not I site and the oligo-dt track which allows
 identification of the library of origin of a clone within
 the mixture. The subtracted library (UI-R-C2) was
 constructed as follows: PCR amplified cDNA inserts from
 UI-R-C1 clones from which 3' ESTs had been derived was
 used as a driver in a hybridization with the UI-R-C1
 library in the form of single-stranded circles. The
 remaining single-stranded circles (subtracted library) was
 purified by hydroxyapatite column chromatography,
 converted to double-stranded circles and electroporated
 into DHI0B bacteria (Life Technologies) to generate the
 UI-R-C2 library. This procedure has been previously
 described (Bernaldo, Lennon and Soares, Genome Research 6:
 791-806, 1996)"

BASE COUNT 86 a 133 c 117 g 128 t

ORIGIN

Query Match 19.1%; Score 318.8; DB 41; Length 464;
 Best Local Similarity 86.9%; Pred. No. 9.1e-52;
 Matches 403; Conservative 0; Mismatches 42; Indels 19; Gaps 4;

QY 1208 agctcgagccggttcgagcgagctcaagcgttcctggtggtcaagaagcagca 1267
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 DB 463 AGCTCGGGCCCGTGGCGGCGAGCTCAAGCAGTTCTCGGCTCAAGAGCACGCG 404
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 QY 1268 tactctgaaacctagttccgctgtacgaccagtgctggtggaagcaagtgca 1327
 |||||||
 DB 403 TACTGCTGAACCTTAGCTTCGCTGTACGACCACTGGCGTCTTGATGCAAGTCA 344
 |||||||
 QY 1328 cacaagaccgaagaccagagaggtatcctgcttcgggacagaggggtgcgagaga 1387
 |||||||
 DB 343 CACAAGACCAGAAACGAGGAGGAGATCCTCGGCGAGACGGGTTGCGCGAGA 284
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QY 1388 gttccctcggttaactctaagatagggccatctcctctgctgggt-cagacctgagac 1446
 |||||||
 DB 283 GGTCTGCGCGCTAAACTGTGAGGATAGGCCATCTCTCTGATGCGAGCTGGAGGC 224
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 QY 1447 tcacctgaattggagccctctgtac-----catctggcaacaaagaaacctaccagag 1501
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 DB 223 TCACCTGAACGTGAGACACATCTGTACTGTACCTTTGGGCAATGAAGAAACAAACGAG 164
 |||||||
 QY 1502 gctggggcacaatgagctccacacacagagcttggctcaatgatgctcaacttga 1561
 |||||||
 DB 163 GCTGGGGCAATGAGCTCCACACACAGCTTGG-CCACATGATGCTCAACTTGA 105
 |||||||
 QY 1562 tatacccaagtggtggttaagttg-----gggatgcaaggccctcccaacaa 1609
 |||||||
 DB 104 TGTACCCCATATAGGTAGGTTGGAGTAATGACAAAGGTTATGACAGACCTCCAGAG 45
 |||||||
 QY 1610 tctcttaataataaaggaggtgttcaggttaaaaaa 1653
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 DB 44 TCTCTTGAAATTAATTAAGAAAGATTAAAAA 1

Search completed: September 28, 1999, 15:38:09
 Job time: 3277 sec

[illegible]

RESULT 2
 US-08-458-568A-11/c
 : Sequence 11, Application US/08458568A
 : Patent No. 5621339
 : GENERAL INFORMATION:
 : APPLICANT: Schaffer, Priscilla A.
 : APPLICANT: Yeh, Lily
 : TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus
 : TITLE OF INVENTION: Infections
 : NUMBER OF SEQUENCES: 15
 : CORRESPONDENCE ADDRESSES:
 : ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5621339r1s
 : STREET: One Liberty Place, 46th floor
 : CITY: Philadelphia
 : STATE: PA
 : COUNTRY: USA
 : ZIP: 19103
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Wordperfect 5.1
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/458,568A
 : FILING DATE: 02-JUNE-1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/065,146
 : FILING DATE: 05-MAY-1993
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Leary Ph.D., Kathlyn R.
 : REGISTRATION NUMBER: 36,317
 : REFERENCE/DOCKET NUMBER: DPCI-0029
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (215) 568-3100
 : TELEFAX: (215) 568-3439
 : INFORMATION FOR SEQ ID NO: 11:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 12001 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (genomic)
 : HYPOTHEetical: NO
 : ANTI-SENSE: NO
 : ORIGINAL SOURCE:
 : ORGANISM: Herpes simplex virus
 : STRAIN: Herpes Simplex Virus Type 1
 : US-08-458-568A-11

	Query March	Best Local Similarity	2.7% 50.2% P: 0.28	Score 45.4	DB 3	length 12001
	Matches 112	Conservative	0	Mismatches 111	Indels 0	Gaps
QY	2	gcacgagcttcgtctgttcgcgcacagtagcgcgtgtgcagaccgagcccaatctgac	61			
Db	4036	gccccgcaccccccctccccgcggcccccctccctccaccccccgggcccgaagccgcgc	3977			
QY	62	ccgcgcagctcgcgcgcgcgcacataccgcggtttgcagtaaccgcgcgtttgcgcacacc	121			
Db	3976	ccccccacagcccccggggcccccggggcccccgcgcgcacagcccccgcgcgcgcgcgc	39171			
QY	122	ccaatgccgcgcggttcgcgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	181			
Db	3916	gtgtcgc	3857			
QY	182	ctgtcgcgcgtgtgtgtgcgcgtctgtgtgcgtctgtgtgcgtctgtgtgcgcgcgcgcgc	224			
Db	3856	gggcgcacagcacacaggggc	3814			

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    2  gacagagcttcgctgctgcgcgcacgtagcgcgttgagaccgcagcccatctgcac 61
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2638 GCCCGCGCCCGCCCTTCCTCCCGCCCGCCCGCCCTTCACAGCCCGCGGCGCCGACCGCCGCG 2697

RESULT 3
US-08-690-473-1
: Sequence 1, Application US/08690473
: Patent No. 5876923
: GENERAL INFORMATION:
: APPLICANT: Leopardi, Rosario
: APPLICANT: Roizman, Bernard
: TITLE OF INVENTION: HERPES SIMPLEX VIRUS TCP4 AS AN
: TITLE OF INVENTION: INHIBITOR OF APOPTOSIS
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/690,473
: FILING DATE: 26-JUL-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Highlander, Steven L.
: REGISTRATION NUMBER: 37,642
: REFERENCE/DOCKET NUMBER: ARCD:239
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512/418-3000
: TELEFAX: 512/474-7577
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4257 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
US-08-690-473-1
Query Match 2.7%; Score 45.4; DB 4; Length 4257;
Best Local Similarity 50.2%; Pred. No. 0.11;
Matches 112; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

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1 APPLICANT: Mu-En Lee
2 TITLE OF INVENTION: TRANSFORMING GROWTH
3 TITLE OF INVENTION: FACTOR- INHIBITS
4 TITLE OF INVENTION: INDUCIBLE NITRIC OXIDE
5 TITLE OF INVENTION: SYNTHASE GENE
6 TITLE OF INVENTION: TRANSCRIPTION
7 NUMBER OF SEQUENCES: 6
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Fish & Richardson
10 STREET: 225 Franklin Street
11 CITY: Boston
12 STATE: Massachusetts
13 COUNTRY: U.S.A.
14 ZIP: 02110-2804
15
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
18 COMPUTER: IBM PS/2 Model 502 or 55SX
19 OPERATING SYSTEM: MS-DOS (Version 5.0)
20 SOFTWARE: Wordperfect (Version 5.1)
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22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: PCT/US94/03705
24 FILING DATE: 5 April 1994
25 CLASSIFICATION:
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER:
28 FILING DATE:
29
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Janis K. Fraser
32 REGISTRATION NUMBER: Reg. No. 34,819
33 REFERENCE/DOCKET NUMBER: 05433/007001
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: (617) 542-5070
36 TELEFAX: (617) 542-8906
37 TELEX: 200154
38
39 INFORMATION FOR SEQ ID NO: 3:
40
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 2745
43 TYPE: nucleic acid
44 STRANDEDNESS: double
45 TOPOLOGY: linear
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47 PCT-US94-03705-3
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1 COUNTRY: USA
2 ZIP: 77210
3
4 COMPUTER READABLE FORM:
5
6 MEDIUM TYPE: floppy disk
7
8 OPERATING SYSTEM: IBM PC compatible
9
10 SOFTWARE: PatentIn Release #1.0, Version #1.25
11
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/08/242,677
14
15 FILING DATE:
16
17 CLASSIFICATION: 435
18
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Mayfield, Denise L.
21 REGISTRATION NUMBER: 33,732
22 REFERENCE/DOCKET NUMBER: UTSD:401
23
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: 713-787-1400
26 TELEFAX: 713-789-2679
27
28 INFORMATION FOR SEQ ID NO: 1:
29
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 5173 base pairs
32 TYPE: nucleic acid
33 STRANDEDNESS: single
34 TOPOLOGY: linear
35
36 MOLECULE TYPE: CDNA
37
38 FEATURE:
39 NAME/KEY: CDS
40 LOCATION: 1..4863
41
42 US-08-242-677-1

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Query Match      2.68;  Score 43.2;  DB 2;  Length 5173;
Best Local Similarity 79.78;  Pred. NO. 0.36;
Matches  51;  Conservative  0;  Mismatches  13;  Indels  0;  Gaps  0;
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Dd	5073	TTTAAATAAATATTTAAGCAATTGCCAATAAAAAAAAAAAAAAAAAAAAA	5132
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Dd	5133	AAAA	5136

RESULT 10
 US-08-467-607-2
 Sequence 2, Application US/08467607
 Patent No. 5783434
 GENERAL INFORMATION:
 APPLICANT: TUNG, JAY S.
 APPLICANT: SINHA, SUKANTO
 APPLICANT: MCCONLOGUE, LISA
 APPLICANT: TATSURO, GWEN
 APPLICANT: ANDERSON, JOHN
 APPLICANT: CHRISLER, SUSANNA
 TITLE OF INVENTION: NOVEL CARPENSIN AND METHODS AND
 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ATHENA NEUROSCIENCES
 STREET: 800 F. Gateway Blvd.
 CITY: South San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,607
 FILING DATE: 06-JUN-1995

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Db 361 GACCCCTCAATGGTCGCCCGCTGCCCTCTGAGCTGTCGCCGCTCTTAAACACCTCCACCT 420
Qy 421 ggcctgcccctgctcaacattatgggtccaggcagcagtcagcagcagcagcagcagcagc 480
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Db 541 GAAGCCCTTAAACATCAGCTGCTGCTGCTCCGGAACATGAAGATCTCACGTGCCGCTGGAC 600
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Qy 841 cccccccagcagctgacgtgagccgctgtggggcctgagagaccagctgagtgatcg 900
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Qy 1501 ggcctggggcaccaatgagctccacacacacagcttgggtccacatgatggtcacactgg 1560
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Db 1621 AAATAAGAGTGTTCAGGTAAAAAATAAAAAAATAAAAAAATAAAAAA 1673

RESULT 2
V41688
ID V41688 standard; cDNA; 1656 BP.
AC V41688;
DT 26-OCT-1998 (first entry)
DE Nucleotide sequence of the murine U4 gene.
KW Murine; U4 protein; haematopoietin receptor superfamily;
KW cell proliferation; immune response; antibody; cell differentiation;
KW autoimmune disease; cancer; allergy; ds.
OS Mus sp.
FH Key Location/Qualifiers
FT 122..1399
FT /*tag= a
FT /product= "U4 protein"
PN WO9831811-A1.
PD 23-JUL-1998.
PF 15-JAN-1998; U00334.
PR 16-JAN-1997; US-784863.
PA (GENY) GENETICS INST INC.
PI Collins M, Donaldson DD, Neben T, Whitters M;
DR WPI: 98-414109/35.
DR P-PSDB: W59804.
PT New nucleic acid encoding U4 haematopoietin receptor superfamily
chain - potentially useful, e.g. for modulating cell proliferation
or immune response, for treating cancer and autoimmune disease
Claim 1; Pages 25-26; 38pp; English.
CC This is the nucleotide sequence encoding the murine U4 protein from
the haematopoietin receptor superfamily, used in the method of the
invention for the modulation of cell proliferation, or the immune
response. Transformed mammalian cells are used to produce recombinant
U4 protein. The U4 protein is used to screen for specific binding
agents, raise antibodies. It is also used as reagents for assays and
as tissue markers for isolation of cognate ligands and receptors, and
in pharmaceutical compositions which may modulate cell proliferation,
cell differentiation, and the immune system (e.g. for treating immune
deficiency, inherited or the result of infection, autoimmune diseases,
cancer, and allergy).
SQ Sequence 1656 BP; 318 A; 552 C; 478 G; 308 T;

Query Match 96.5%; Score 1614.6; DB 1; Length 1656;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1634; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

Qy 5 cgagcttcgcttcgagcccgagtcgagcagtcgagcagtcgagcagtcgagcagtcgagc 64
Db 3 CGACCTTCGCTGTCGCCCGCCACAGTACGCGCGGTGAGGACCCGAGCCCCCAATTTGACCCC 62
Qy 65 gtagactcgcccccgc 124
Db 63 GCAGACTCGCCCCCGCCCCATACCGGCGTGTGAGTCACCGCCCGTGTGCGCGCACCCCC- 122
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/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: lung; Vector: pT7T3p (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGACGTGGAGCGCGCAATTTTTTTTTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NbHL19W."
68 a 169 c 122 q 72 t

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BASE COUNT      68 a      169 c      72 t
ORIGIN          recu      medu      nunnaw..

Query Match      19.4% ; Score 324.2 ; DB 45; Length 431;
Best Local Similarity 85.3% ; Pred. No. 8.4e-53;
Matches 362; Conservative 0; Mismatches 63; Indels 0; Caps 0;

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[illegible]

RESULT	14
LOCUS	A1233311/c
DEFINITION	EST
ACCESSION	A1233311
NID	9387191
VERSION	A1233311.1
KEYWORDS	GI:3817191
SOURCE	EST.
ORGANISM	Rattus sp. Rattus sp. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 470)
REFERENCE	Lee N.H., Glodek.A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
AUTHORS	Rat Genome Project: Generation of a Rat EST (RESt) Catalog & Rat
TITLE	

Gene Index
JOURNAL
COMMENT

On May 8, 1995 this sequence version replaced gi:801255.

Contact: Lee, NH
ATCC
The Institute for Genomic Research
9713, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.

location/Qualifiers
1. .470
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RK1DD49"
/clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"

BASE COUNT 88 a 143 c 124 g 115 t
ORIGIN

Query Match	19.3%	Score 323.4	DB 43	Length 470
Best Local Similarity	87.2%	Pred. No. 1.2e-52		
Matches 407	Conservative	0	Mismatches 41	Indels 19
Gaps				
1188	agccgcggggcgagccagctcgccgcggctgcgcgcgagctcaagcagttctctg	1247		
Db	470	AACCGGGGGCGGAGCATAGCTCGGCCCGGTCGGCGAGCTCAAGCAGTTCCTCG	411	
QY	1248	gtcgctcaagaagcacgcatactctcgaaaccttagttccgcctgtacgaccagttg	1307	
Db	410	GTGTGCTCAAGAAGCACGCTACTCTCGAACCTTAGTCTCGGCTGTACGACCAGTGGC	351	
QY	1308	gtgcttgatgcagaagtcacacaagaccggaaccaggacgagggatcctgcctcgg	1367	
Db	350	GTGCTTGATGCAGAGTTCACACAGACCCGAACCCAGCAGGGGATCTCGCCCTCGG	291	
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Db	290	GCAGACGGGGTTCGGCGAGAGTCTCTCGCGCTAACTCTGAGATAGGCCATCTCCTG	231	
QY	1428	ctggggt- cagacctgaggtctcacctgaatggagccctctgtac-----catctgggc	1481	
Db	230	CTGGATGCAGACCTCGGAGGCTACCTGTAACTTGGAGACCATCTGACTGTCACTTGGGGC	171	
QY	1482	asacaagaacctcagaggtcggggcacaatgagctcccaacacacagctttgttc	1541	
Db	170	AATGAAGAACAACACAGGGGCTGGGCGACAAATAGTCCCAACACACAGCTTTGG-CC	112	
QY	1542	acatgatgtcacacttgatatacccccaggtgggtaaggttg-----gggt	1589	
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RESULT	15
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LOCUS	AIO71408
DEFINITION	UI-R-C2-nb-d-08-0-VI.s1 UI-R-C2 Rattus norvegicus CDNA clone
ACCESSION	U01964
NID	93397623
VERSION	AIO71408.1
KEYWORDS	EST.
SOURCE	Norway rat.
ORGANISM	Rattus norvegicus
	Eukaryota; Metazoa;
	Cnidaria; Vertebrata; Mammalia;
	Chordata; Eumetazoa; Chordata; Craniata; Vertebrata; Mammalia;
	Mammalia; Rodentia; Muridae; Murinae; Murini; Rattus; Rattus norvegicus
	EST
	mRNA
	464 bp
	11-FEB-1999

QY 1351 ggggatactctcttccggcagacgggtggtggcgagaggtctctccggttaaaacttaag 1410
 Db 125 GGGGATCTCGCCCTC-GGCAGACGGGTGGCGCAGAGGTCTCTCCGGCTAAATCTTAAG 183
 QY 1411 gatggccatct 1470
 Db 184 GATAGGCATCT 243
 QY 1471 accatctggcacaacaaagaaactaccagaggtctggggcacaatgaagctcccaaacac 1530
 Db 244 ACCATCTGGGCAACAAAGAAACCTTACCAGAGGCTGGGGCAATGAGCTCCCAACACC 303
 QY 1531 agcttggctccacatgatggtccacacttgatatacaccacagtg--tggttaaggttgagg 1588
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 Db 364 TATTGCAGGGCTCCCAAGAGTCTTT 390
 RESULT 12
 A1187074 447 bp mRNA EST 29-OCT-1998
 LOCUS qe38a03.s1 Soares_fetal_lung_NbHL19W Homo sapiens CDNA clone
 DEFINITION IMAGE:1741228 3', mRNA sequence.
 ACCESSION A1187074
 NID 3737712
 VERSION A1187074.1 GI:3737712
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 447)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT On Aug 21, 1998 this sequence version replaced.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
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 High quality sequence stop: 431.
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 /db_xref="taxon:9606"
 /clone="IMAGE:1741228"
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 /dev_stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: lung; Vector: p773D (Pharmacia) with a
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(GT) primer
 [5'-TGTTACCAATGAGTGGGAGCGGCCCAATTTTCTTTTCTTTT-3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified p773 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo. This library was constructed
 from the same fetus as the fetal heart library, Soares
 fetal heart NbHL19W."
 69 a 175 c 128 g 74 t 1 others

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 Db 61 CGGATCAGGAGGCCACACAGCTGTGATCAGTCCCGAGGATCCACACGCTTCTCATCGGCTC 120
 QY 295 ctccctgcaagtact 354
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 Db 421 CTGGACGCCAGGGGCCCGCCGNGAGAC 447
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 NID 94070371
 VERSION A1333812.1 GI:4070371
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 431)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT On Jan 14, 1998 this sequence version replaced gi:1797892.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1615 Std Error: 0.00
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 High quality sequence stop: 407.
 Location/Qualifiers
 1..431
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 /clone="IMAGE:1930606"

BASE COUNT
 ORIGIN

REFERENCE	1 (bases 1 to 466)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	On Jan 19, 1998 this sequence version replaced gi:2151491.
CONTACT:	Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov
DESCRIPTION:	This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1622 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 466.
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BASE COUNT	79 a 183 c 123 g 80 t 1 others
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Best Local Similarity	85.6%; Pred No. 1.8e-58;
Matches 393; Conservative	0; Mismatches 66; Indels 0; Gaps 0;
QY	199 gcctcgttgctctgtgcttcctcggggtgcctcggggcgagccgccacagctgt 258
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QY	259 aaacgccccaggaccaccttctcatcggtctccctccaagtactcctcttat 318
Dd	
Dd	67 GATCAGTCCCAGGATCCCCAGCTTCTCATCGGCTCTCGCTGTGTCACCTGCTCAGT 126
QY	319 acattgagacacactggggcccacgcctgaggggcttaactgaacctcaatggcgccg 378
Dd	
Dd	127 GCAGGAGACCACAGGAGCCACCGCCGAGGGGCTCTACTGGACCTCAACGGGCGCG 186
QY	379 cctgccccttgagctgtcccgccctcttaaacctcacacctcgcctggccctggcgtaa 438
Dd	
Dd	187 CTRGCCCCCTGAGCTCTCCCGTGTA CTACGGCTCCACCTTGGCTCTGGCCCTGGCCAA 246
QY	439 cctaataatgggtccaggcagtcaggagacaacttgtgtgtacgccccgagacggcag 498
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QY	499 cattctggctggctcctcctctattgttgcttgccccctgagaagccctttaaatcag 558
Dd	
Dd	307 CATCTCGGTGGCTCTCTGCTCTCTATGTTGGCCCTGCCCCAGAGAAGCCGCTCAACATCAG 366
QY	559 ctgctgggtcccgaaacatgaagatctcacgtgcctgtagacacccgggtgcacacggga 618
Dd	
Dd	367 CTGCTGGTCCAAGAACATGAAGAC TTGACCTGCCGCTGGAGCCGAGGGGCCCACGNGA 426
QY	619 gacattcttacataccaactactccctcaagtacaagct 657
Dd	

BASE COUNT	ORIGIN
79 a	Soares and M. Fatima Bonaldo.
181 c	79 t
122 g	1 others

Query Match	21.2%	Score	355.4	DB	45	Length	462
Best Local Similarity	85.5%	Pred. No.	9.5e-59				
Matches	395	Conservative	0	Mismatches	57	Indels	0
						Gaps	0

196	Qy	gtcgctctgttgcctctgtctcctcggggtcctcggggcgagatcgggagccacacagc	255
1	Db	GCCCCTGCTCTCTCTGCGTCTCTGGGCGCGCGAGCGGATCAGGAGCCACACAGC	60
256	Qy	tgtaatcagccccagagaccccaacctctcatcggctctcctcctcgaagctacactgtcc	315
61	Db	TGTGATCAGTCCCACGAGATCCCACGTTTCTCATCGGCTCCTCCCTGCTGGCCACCTGTCTC	120
316	Qy	tatacatggagacacacctggggccaccgcctgaggggtctctactgaccctcaatggtag	375
121	Db	AGTGACGGAGATCCACCAGAGGCCACCGCGGAGGGCCTCTACTGAGCCCTCAATGGGGG	180
376	Qy	ccgcctcctcttgagctctcccgccctcttaacacctccacctggccctgagccctgpc	435
181	Db	CCGCGCTCCCCCCTGAGCTCTCCCGTGACTCAACGGCTTCACCTTGGCTCTGGCCCTGGC	240
436	Qy	taaccttaatgggtccagggcagcagtcagagagacaactctggtagtcacagcccgagacgg	495
241	Db	CAACCTCAATGGGTCCAGGCAGCGGTGGGGGGACAACCTCTGTGTGCCACGCCGCTGACGG	300
496	Qy	cagcaatctggctggctcctctctatgtttgcttgccccctgagaagccctttaaat	555
301	Db	CAGCATCTGGCTGGCTCTGCGCTCTATGTGGCTCGCCCCAGAGAAACCGCTCAACAT	360
556	Qy	cagctgtgtctcccggaacatgaaggatctcacgtgcgctgacaccgggtgcacacgg	615
361	Db	CAGTGTGTGTTCAAGAACATGAGGACTTGACCTGCGGCTGAGCGCCAGGGGGCCACGG	420
616	Qy	ggagacattcttacataccaactactcctcctaagtacaagct	657
421	Db	NGAGACCTTCTCTCCACACCAACTACTCCCTCAAGTACAACT	462

RESULT 9
 A1161002
 LOCUS
 DEFINITION
 ACCESSION
 NID
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 466)
 NC1-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 Tumor Gene Index
 Unpublished (1997)
 On Jan 19, 1998 this sequence version replaced qi:2287379.
 JOURNAL
 COMMENT

Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 1599 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 454.
 Location/Qualifiers
 1. .466
 /organism="Homo sapiens"
 FEATURES
 source

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/db_xref="taxon:9606"
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/clone="IMAGE:1705398"
/clone_lib="Soares.fetal_heart_NBHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: heart; Vector: pT7m3D (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCGGCACATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHL19W."
79 a 183 c 123 g 80 t 1 others

```

	Query Match	21.28;	Score 354;	DB 43;	Length 466;
	Best Local Similarity	85.6%;	Pred. No. 1.8e-58;		
	Matches 393;	Conservative 0;	Mismatches 66;	Indels 0;	Gaps 0;
Qy	199	gcctctgttgcctgtcctcgcgggtgcctcgcgggcggtatcgggagccacacagctgt	258		
Db	7	GCTGCTGTGCTCTGCGTCTCGGGGCCCGCGAGCCGGATCAGAGGCCACACAGACTGT	66		
Qy	259	aatcagccccagagccccacccttctcatcgggtcctccctcctgcagctacctgtctct	318		
Db	67	GATCAGTCCCAGGATCCACGCCTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTCACT	126		
Qy	319	acatggagacacacacctggggccacgcgtgaggggtctactcggaccctccaatggtcgccg	378		
Db	127	GCACGGAGACCCACCAGGAGCACCGCGGAGGGCCCTCTACTGGACCCCTCAACGGGCGCG	186		
Qy	379	cctgcctctctgagctgttcgcgcctcctttaaaccctccacctggccctggccctggctaa	438		
Db	187	CTGTGCCCTTGAGCTCTCCGCTGTACTCAACGCTCCACCTTGGCTCTGGCCCTGGCCAA	246		
Qy	439	ccttaatgggtccagcagcagtcagagagacaatcgtgtgtcaccgcccgagcgcgag	498		
Db	247	CTCTAATGGGTCCAGGACGGTTCGGGGGACAACTCTGTGTCCACGCCCGTGTACGGCAG	306		
Qy	499	cattctggctgcctcgtcctctatgttggcttgcctccctcgcagagcccttaacatcag	558		
Db	307	CATCCTGGCTGCTCCTGCCTCTATGTGTGGCTGTGCCCCAGAGAAACCCGTCAACATCAG	366		
Qy	559	ctgctggttcocggaaatgaaggatctcactcgtgcgcgtggacacacccgggtgtcacacggga	618		
Db	367	CTGCTGGTCCAAAGACATGAAGGACTTGAACCTTGCCTGCGCTGGAGCCAGGGGCCACGGNGA	426		
Qy	619	gcattcttaataccaactactcctcgaagtacaagct	657		
Db	427	GACCTTCTCCACCAACTACTCCTCAAGTACAAGT	465		

RESULT	10
AII185780	
LOCUS	AII185780 466 bp mRNA EST
DEFINITION	ge44h04.xl Soares_fetal_lung_NbHL19W Homo sapiens CDNA clone
IMAGE:	1741879 3', mRNA sequence.
ACCESSION	AII185780
NID	93736418
VERSION	AII185780.1 GI:3736418
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
	Eutheria; Primates; Catarrhini; Hominidae; Homo

```

RESULT 7
AI185924 477 bp mRNA EST 29-OCT-1998
LOCUS qe50c05.x1 Soares fetal lung NBHL19W Homo sapiens cDNA clone
DEFINITION IMAGE:1742408 3' similar to TR:Q16354 Q18334 PROLACTIN RECEPTOR ;
mRNA sequence.
ACCESSION AI185924
NID 93736562
VERSION AI185924.1 GI:3736562
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 477)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Feb 17, 1998 this sequence version replaced gi:2150926.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1552 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 467.
Location/Qualifiers
1..477
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1742408"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: lung; Vector: p773D (Pharmacia) with a
modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTACCAATCAAGTGGAGCGCGCAATTTTCTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p773 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NBHL19W."
BASE COUNT 81 a 183 c 129 g 83 t 1 others
ORIGIN

Query Match 21.7%; Score 362.8; DB 43; Length 477;
Best Local Similarity 85.6%; Pred. No. 3.7e-60;
Matches 403; Conservative: 0; Mismatches 68; Indels 0; Gaps 0;

QY 199 gctctgttgcctgtcctcgggggctcctcggggcgatcgaggagccacacagctgt 258
Db 7 GCTGCTGCTGCTCGGCTCGGGGGCGCGCGGATCGAGCGCCACACAGCTGT 66
QY 259 aatcagccccagaccacccctctcctcgcctcctcctcgaagctactctctat 318
Db 67 GATCAGTCCCAGGATCCCAGCTTCTCATCGGCTCCCTCCCTGCTGGCCACTGCTCAGT 126
QY 319 acatggagacacctggggccaccgctgagggggctctactggaccctcaatggtcgccg 378
Db 127 GCACGGAGACCCACACGAGCCACCGCGGAGGGGCTCTACTGGACCCTACAGGGCGCCG 186
QY 379 cctgcctctgagctgtcccgctcctcttaaacacctcaccctggcctggcctggttaa 438
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 187 CTTGCCCCCTGAGCTCTCCGCTGACTCAACGCCCTCCACCTTGGCTCTGGCCCTGGCCAA 246
QY 439 ccttaattgggtccaggcagcagtcaggagacaatctggtgtgtcagccgagagcggcag 498
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 247 CCTCAATGGTCCAGCAGCGTCCGGGGACAACTCGTGTGCCACGCCGCTGACGGCAG 306
mRNA sequence.
QY 499 cattctgggtgctcctcctctatgttgcttgcctcctgagaagcccttttaacatcag 558
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 307 CATCTGGTGGCTCTCTGCTCTATGTGGCTCGCCCGCAGAGAAACCGGTCAACATCAG 366
QY 559 ctgctgggtcccggaacatgaagatctcacgtgcgcgtgggacacccgggtgcacacgggga 618
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 367 CTGCTGGTCCAAAGAACATGAAGGACTTGACCTGCCGCTGGAGCCAGGGGCCACCGNGA 426
QY 619 gacattttacatacacactactcctcaagtcacagtgaggtggtgacgg 669
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 427 GACCTTCCTCCACACCACACTACTCCTCAAGTACAAAGCTTAGGTGCTATGG 477
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RESULT 8
AI394468 462 bp mRNA EST 30-MAR-1999
LOCUS tf79d12.x1 NCI-CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105495 3',
DEFINITION mRNA sequence.
ACCESSION AI394468
NID G4224015
VERSION AI394468.1 GI:4224015
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 462)
REFERENCE NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
TITLE (CGAP/BTGP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT On Feb 17, 1998 this sequence version replaced gi:2887603.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1631 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 454.
Location/Qualifiers
1..462
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/db_xref="taxon:9606"
/map="10;1"
/clone="IMAGE:2105495"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/notes="Organ: brain; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCAAGTGGAGCGCGCAATTTTCTTTT-3']; double-stranded
cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p773 vector.
Library is normalized, and was constructed by Bento

```


/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; This library
consists of a mixture of individually tagged normalized
libraries constructed from rat placenta, adult lung,
brain, liver, kidney, heart, spleen, ovary, and muscle.
The tag is a string of 3-5 nucleotides present between the
Not I site and the oligo-dr track which allows
identification of the library of origin of a clone within
the mixture."
87 a 134 c 120 g 87 t

BASE COUNT 87 a 134 c 120 g 87 t
ORIGIN
Query Match 23.4%; Score 391.8; DB 45; Length 428;
Best Local Similarity 94.8%; Pred. No. 1.1e-65;
Matches 405; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 660 ggtgtacggtcaggataacacatgtgagtgagtgaccacactgtggccctcactcatgcc 719
Db 2 GCGCGCTCAATCAGGACACACATGTGAGGNATATCATCTGGTGGGCCCTCCTGCGC 61
QY 720 atatcccaaggacctggccctcttccactccctatgatgtggtggaagccaccatc 779
Db 62 ATATCCCAAGACCTGGCCCTCTTACGCCCTATGAGATCTGGGTGGAAGCCACCAATC 121
QY 780 gcttagctcgaagatctgattctcctacactggatgtctctgagtgagtgaccacgg 839
Db 122 GCTGGGTTCAGCAGATCTGACGTGCTCACACTGGATGTCTCTGGACGTGTGACACGG 181
QY 840 accccacacgacgtcacgtgacgcgctgtggggcctgagagaccagctgagtgctgc 899
Db 182 ACCCTCCACCCAGCTGCACGTGACGCCGCTGGGGCCCTGGAGACGAGTGTGCTGC 241
QY 900 gctgggtctcaccacagctctcaaggatttctctcttccaaagccaagtaccagatccgct 959
Db 242 GCTGGGTCTACCCAGCAGCTCTCAAGGATTTCTCTTCCAAAGCCAAATACAGATTGCT 301
QY 960 accgctgagagacagctgagctgagtgagtggtggtgagtgagtgagtgagtgagtg 1019
Db 302 ACCGCTGGAGGACAGCGTGGACTGGAAAGTGGTGGATGAGTGCAGTGCAGCAACGACCTCT 361
QY 1020 ccgctctcggggcctgaagccgacccgaccccttactctgctcaagtcggtgtaacccat 1079
Db 362 GCGGTCTCGCGGGCTTGAAGCCGCGACCTTTACTTCTGTCGAAGTTCGTTGTATACCAT 421
QY 1080 tgggat 1086
Db 422 TCGGAT 428
RESULT 6
AI421423 474 bp mRNA EST 30-MAR-1999
LOCUS tf25h01.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2097265 3'
DEFINITION similar to SW:IL6B_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN
PRECUSOR ;, mRNA sequence.
ACCESSION AI421423
NID 94267354
VERSION AI421423.1 GI:4267354
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 474)
AUTHORS NCI/NIHDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGA), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT On Apr 7, 1998 this sequence version replaced gi:3034955.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbbrp/image/image.html

Insert Length: 1664 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 450.
Location/Qualifiers
1. .474

FEATURES
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/clone="IMAGE:2097265"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"

/notes="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dr) primer [5'
TGTACCACTCTGAAGTGGAGCGCGGCATATCTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 81 a 181 c 128 g 83 t 1 others
ORIGIN

Query Match 21.8%; Score 364.2; DB 46; Length 474;
Best Local Similarity 85.4%; Pred. No. 2e-60;
Matches 405; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 196 gtcgctctgtgtgtctgtctgtctgtctgtctgtctgtctgtctgtctgtctgtctgt 255
Db 1 GCCCTGT 60
QY 256 tgtaatacagccccagagacccccctctctctgtctgtctgtctgtctgtctgtctgtct 315
Db 61 TGTGATCAGTCCCGAGGATCCACGCTTCTCATCGGCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 316 tatacatggagacacacctggggccacgcgtgaggggctctactggagccctcaatggtcg 375
Db 121 AGTGCAGGAGACCCACCAGGAGGACCCGCGAGGGGCTCTACTGGAGCCCTCAATGGGCG 180
QY 376 ccgctgctctgt 435
Db 181 CCGCTGCCCCCTGAGCTCTCCGCTGTACTCAAGCCCTCCACCTTGGCTCTGGCCCTGCG 240
QY 436 taaccttaatgggtccagggcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 495
Db 241 CAACCTCAATGGTCCAGGACGCGTCCGGGGGACAAACCTCGTGTGCCACGCCCGTGACGG 300
QY 496 cagcatttgggt 555
Db 301 CAGCATCTGGCTGGCT 360
QY 556 cagctgt 615
Db 361 CAGCTGT 420
QY 616 ggagacattcttatacaccactcctcctcaagtacaagctgaggtgtgtgtgtgtgtgt 669
Db 421 NGAGACCTTCTCTCCACACCAACTACTCTCTCAAGTACAAGCTTAGTGTGTGTGTGTGG 474

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QY 1536 tggctccatgatggtcaccacttgat 1562
Db 27 TGGTCCACATGATGGTCACACTGGAT 1

RESULT 4
AA039053/c 445 bp mRNA EST 29-AUG-1996
LOCUS m199d07.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus cDNA
DEFINITION clone IMAGE:474733 5', mRNA sequence.
ACCESSION AA039053
NID g1514788
VERSION AA039053.1 GI:1514788
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS 1 (bases 1 to 445)
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Matra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:285477
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 441.
Location/Qualifiers
1. 445
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="474733"
/clone_lib="Soares mouse embryo NBME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/notes="vector: p7T73d-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dt) primer [5',
TGTACCAATCTGAAGTGGAGCGGCGCGGAATTTTGTGTGTGTGTGTGTGTGTGTGT
T 3'], on equal amounts of mRNA from 2.13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."
BASE COUNT 85 a 129 c 124 g 107 t
ORIGIN

Query Match 25.78; Score 430.6; DB 27; Length 445;
Best Local Similarity 98.08; Pred. No. 4.3e-73;
Matches 436; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1207 cagctggcccggtggtcgagctcaagcagttctcgtcggtcgaagcagc 1266
Db 445 CAGCTCGGCGCGGTGGCGCGGAGCTCAGCAGTTCTCGGCTCGGCTCAGAGCAGC 386

```

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QY 1267 atactgctcgaaaccttagtttccgcctctacgaccagtggtgcttggatgcagaagtc 1326
Db 385 ATACTGCTCGAACCCTTAGTTTCCGCCTGTACACCAGTGGCGTGTGGATGCAGAAGTC 326

QY 1327 acacaagcccgaaaccaggagggggtatcctgcttcgggagcagcgggtggtggtggcag 1386
Db 325 ACACAAGACCCCGAAACACAGGAGGAGGATCTCGCTCCGCGAGACGGGTGGCGGAG 266

QY 1387 aggtcctccgggttaaaccttaagatagggcaccatcctcctggtggtcagacctggagggc 1446
Db 265 AGGTCTCTCCGGCTAAACTCTAAGGATAGGCATCTCTCTCTGCTGGGTGAGACCTGGAGGC 206

QY 1447 tcacctgaattggagccctctgtaccatctgggcaacaagaacacctaccagaggtgtg 1506
Db 205 TCACCTGATTTGGAGCCCTCTGTACCATCTGGGCACAAAGAACCTTACCAGAGGTGG 146

QY 1507 ggcacaatgagctcccaacacacagcttgggtccacatggtggtcacttgatgatac 1566
Db 145 GGCACAATGAGCTCCCAACACACAGCTTTGGTCCACATGATGTCACACTTGGATATAC 86

QY 1567 cccagtgggttaaggttgggttattgcaggggccctcccaaatctctttaaataataa 1626
Db 85 CCCAGTGTGGGTAGGTTGGGTATTGTCAGGGCCTCCCAAGAGTCTCTTTAAATAATAA 26

QY 1627 aggagttgttcagggtaaaaa 1651
Db 25 AGGAGTTGTTCAGGTCCCGAAAAA 1

RESULT 5
AA866388 428 bp mRNA EST 05-FEB-1999
LOCUS UI-R-A0-aj-f-04-0-UI.3 UI-R-A0 Rattus norvegicus cDNA clone
DEFINITION UI-R-A0-aj-f-04-0-UI 3' similar to gBAC003112/AC003112 Human DNA
from chromosome 19 specific cosmid R30292, genomic sequence,
complete sequence [Homo sapiens], mRNA sequence.
ACCESSION AA866388
NID g4230568
VERSION AA866388.1 GI:4230568
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 428)
REFERENCE Bonaldo, M.F., Lennon, G. and Soares, M.B.
AUTHORS Normalization and subtraction: two approaches to facilitate gene
TITLE discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97041477
COMMENT On Mar 16, 1998 this sequence version replaced gi:2961849.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Oligo-dt track not found. Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics
Seq primer: M13 Forward.
Location/Qualifiers
1. 428
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/map="between D1S1765 and UGB"
/clone="UI-R-A0-aj-f-04-0-UI"
/clone_lib="UI-R-A0"

```

14.5dpc embryos [total RNA provided by Minoru KO, Wayne State Univ., from 2]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo.

BASE COUNT 96 a 138 c 147 g 101 t
ORIGIN

Query Match 27.4%; Score 457.8; DB 26; Length 482;
Best Local Similarity 99.4%; Pred. No. 2.8e-78;
Matches 470; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 665 tacgtcaggataaacacatgtgaggtaccacacatgtggccctcactcatgcataatc 724
|||||
DB 482 TACGTCAGGATAACACATGTGAGGAGTACCACATGTGGGCCCTCACTCATGCCATATC 423
|||||
QY 725 cccaaggacctggccctctcactccctatgatctctgggtggagccacacaaatgccta 784
|||||
DB 422 CCCAAGGACCTGGCCCTCTTCACTCCCTATGAGATCTGGTGGAAAGCCACCAATCGCCTA 363
|||||
QY 785 ggtcagcaagatctgatctcctcactggtatgctcctggaactgtgtacacgacccc 844
|||||
DB 362 GGCTCAGCAAGATCTGATGTCCTCACATGTGATGTCCTGGAGCGTGTGACCAAGACCC 303
|||||
QY 845 ccaccgacgtcagctgagcgcgcttggggcctggagaccagctgagttgcctgg 904
|||||
DB 302 CCACCGGACGTCAGCTGAGCGCGCTGGGGCCCTGGAGGACCACTGATGTGGCTGG 243
|||||
QY 905 gtctcacaccagctctcaagattctctcttcccaagccaagtacag-atccgtacgg 963
|||||
DB 242 GTCTCACCACCAAGCTCTCAAGATTTCCTTCCCAAGCAAGTACCAGTATTCGTTACCG 183
|||||
QY 964 cgtgaggacacgtgtgagctgaagtggtggtgatcagtcagcaacacagacctctgcg 1023
|||||
DB 182 CBTGGAGGACGCTGAGTGAAGGTGTGGATGACGTCACCAACCAAGACCTCTCTGGCG 123
|||||
QY 1024 tctcgggacctgaagcccgccacgtttactctgcccaagtcgcttgaacccattcgg 1083
|||||
DB 122 TCTCGCGGCGCTGAAGCCCGGACCGTTACTTCTGCTCAAGTGGCTGTGAACCATTCGG 63
|||||
QY 1084 gatctatgggtcgaaagccgggaatctggagcagtgagtgagccaccccccacg 1136
|||||
DB 62 GATCTATGGTCAAAAAGCGGGAATCTGGAGCGAGTGGAGCCACCCCATCG 10
|||||

RESULT 3
AA049278/c
LOCUS
DEFINITION AA049278 503 bp mRNA EST 30-DEC-1996
m145c04.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus CDNA
clone IMAGE:479046 5', mRNA sequence.

ACCESSION AA049278
NID 91755309
VERSION AA049278.1 GI:1755309
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 503)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lehnon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT On Dec 30, 1996 this sequence version replaced gi:1528949.
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:289790
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 486.

FEATURES

source 1. 503
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:479046"
/clone_lib="Soares mouse embryo NBME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; primer [5', TGTACCAATCTGAGTGGAGCGCGCGAATTTTTTTTTTTTTTTT TGTACCAATCTGAGTGGAGCGCGCGAATTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru KO, Wayne State Univ., from 2]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 85 a 158 c 154 g 106 t
ORIGIN

Query Match 26.9%; Score 449.4; DB 29; Length 503;
Best Local Similarity 98.0%; Pred. No. 1.1e-76;
Matches 497; Conservative 0; Mismatches 6; Indels 4; Gaps 4;

QY 1056 tcgtccaagtctgttaaccattcgggtatctatggtcgaagcgggaatctgga 1115
|||||
DB 503 TCGTCCAAAGTGGTGTAAACCATTCGGGATCTATGGTCAAGAAAGCGGGAATCTGGA 444
|||||
QY 1116 gcgagtggagccacccaccgctgctccacccctcgaagtgcgcccggccggcg 1175
|||||
DB 443 GCGAGT-GAGCCACCCACCGCTGCTCCACCCCTCGAAGTGA-TGGCCGGCCCGGGCG 386
|||||
QY 1176 gcggggtgtgcgagccgcgggcgagccagctcgggcccgtgcggcgagctca 1235
|||||
DB 385 GCGGGGTGTGC-CGACGCGGGGCGCGCA-CGCAGCTCGGGCCGCTGCGCGCGAGCTCA 328
|||||
QY 1236 agcagttcctcgtggtctcaagaagcagcagatactgctcgaaccttagttccgctgt 1295
|||||
DB 327 AGCAGTCTCTCGGCTGGCTCAAGAAGCAGCATACTGCTCGAACCTTAGTTTCCGCTGT 268
|||||
QY 1296 acgaccagtgcgtctggatgcagagtcacacacaccccaacagcagagggga 1355
|||||
DB 267 ACACACAGTGGCGTCTTGATGTCAGAGTCAACAGACCCGAAACAGGAGGAGGGA 208
|||||
QY 1356 tctcgtcttcggcgagcgggtgcggcgagaggtcctcgggttaaccttaaggatag 1415
|||||
DB 207 TCTTGCCTCGGACAGCGGGGTGCGCGAGAGGTCTTCCGGCTAAACTCTAAGGATAG 148
|||||
QY 1416 gcatctcctcgtcgttcagacctggaggtcactgaatggagccctctgtacct 1475
|||||
DB 147 GCATCTCTCTGCTGGGTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 88
|||||
QY 1476 ctgggcaacaagaacctaccagaggtctgggcaaatgagctcccaacacagctt 1535
|||||
DB 87 CTGGGCAACAAAGAAACCTTACCAGAGGCTGGGGCAATGAGCTCCCAACACAGCTT 28
|||||

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 28, 1999, 15:38:03 ; Search time 2095.87 Seconds
(without alignments)
1574.548 Million cell updates/sec

Title: US-09-037-657-14
Perfect score: 1873
Sequence: 1 ggcacgagcttcgtctccg.....aaaaaaaaaaaaaaaaaaaaa 1673

Scoring table: IDENTITY_NUC
Searched: 2546578 seqs, 986266752 residues

Database :
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2: em_est2.*
3: em_est3.*
4: em_est4.*
5: em_est5.*
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11: em_est11.*
12: em_est12.*
13: em_est13.*
14: em_est14.*
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16: em_est16.*
17: em_est17.*
18: em_est18.*
19: em_est19.*
20: gb_est1.*
21: gb_est2.*
22: gb_est3.*
23: gb_est4.*
24: gb_est5.*
25: gb_est6.*
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53: em_est21.*

54: em_est22.*
55: em_est23.*
56: em_est24.*
57: em_est25.*
58: em_est26.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	464	27.7	464	29	AA049280 mj45d02.r
2	457.8	27.4	482	26	W66776 mel17b11.r1
3	449.4	26.9	503	29	AA049278 mj45c04.r
4	430.6	25.7	445	27	AA039053 ml199d07.r
5	391.8	23.4	428	45	AA866388 UI-R-A0-a
6	364.2	21.8	474	46	AI421423 tf25h01.x
7	362.8	21.7	477	43	AI185924 qe50c05.x
8	355.4	21.2	462	45	AI394468 tf79d12.x
9	354	21.2	466	43	AI161002 qb69g04.x
10	354	21.2	466	43	AI185780 ge44h04.x
11	343.4	20.5	390	26	WI7583 mb75b01.r1
12	334	20.0	447	43	AI187074 qe38a03.s
13	324.2	19.4	431	45	AI333812 qp93e12.x
14	323.4	19.3	470	43	AI233311 EST229999
15	318.8	19.1	464	41	AI071408 UI-R-C2-n
16	311.4	18.6	417	44	AI269388 q126b05.x
17	296.8	17.7	332	48	AI579568 UI-R-GO-u
18	284.4	17.0	319	48	AI574687 UI-R-GO-u
19	284.2	17.0	385	50	AI670108 we5f03.x
20	246.4	14.7	410	27	AA042914 zk56f01.s
21	215.6	12.9	262	50	AV032198 AV032198
22	204.8	12.2	227	30	AA270365 va83h12.r
23	202	12.1	235	48	AI575060 UI-R-GO-u
24	195.2	11.7	458	27	AA043001 zk56f01.r
25	191.2	11.4	465	26	W46604 zc32h10.s1
26	185.8	11.1	273	23	R87407 ym88d09.s1
27	172	10.3	229	49	AV010798 AV010798
28	149.4	8.9	167	49	AV011309 AV011309
29	148.8	8.9	404	42	AI074921 oy04d08.s
30	144	8.6	455	46	AA925924 UI-R-A1-e
31	143.6	8.6	247	32	AA377893 EST90550
32	131.8	7.9	218	22	H14009 EST00035 Ch
33	129.8	7.8	237	25	N78873 zbl17h05.s1
34	109.8	6.6	234	47	AI535068 UI-R-C3-s
35	105.6	6.3	469	40	AA922128 om45e12.s
36	85.8	5.1	467	29	AA127694 zk89c11.r
37	71.4	4.3	394	40	AA927378 om27a08.s
38	62	3.7	431	28	AA121532 zk89c11.s
39	56.8	3.4	1138	45	AI374006 SNOVAFCAP
40	56.6	3.4	107	27	AA014965 mh23e02.r
41	56.2	3.4	398	44	AI264328 q109c05.x
42	56.2	3.4	389	46	AI417616 tg80c02.x
43	52.4	3.1	641	45	AI357868 qv13b02.x
44	51.6	3.1	1056	26	W42205 mc69e09.r1
45	50.6	3.0	729	39	AA849564 EST192331

ALIGNMENTS

RESULT 1

AA049280
LOCUS AA049280 464 bp mRNA
DEFINITION mj45d02.r1 Soares mouse embryo NME13.5 14.5 Mus musculus cDNA
clone IMAGE:479043 5' similar to SW:IL6B_MOUSE Q00560 INTERLEUKIN-6
RECEPTOR BETA CHAIN PRECURSOR ; mRNA sequence.
ACCESSION AA049280
NID g1755311

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 464)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
On Sep 12, 1996 this sequence version replaced gi:1404537.

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9585
Email: msoares@blue.weeg.uiowa.edu

The sequence tag present in the cDNA between the NotI site and the
oligo-dr track served to identify it as a clone from the normalized
adult lung library. cDNA Library Preparation: M. Fatima Bonaldo,
Ph.D. Clone distribution: clones will be available through Research
Genetics

Seq primer: M13 Forward.
Location/Qualifiers
1. .464
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C2-nb-d-08-0-UI"
/clone_lib="UI-R-C2"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-C2
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the
UI-R-C0 library. The UI-R-C0 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dr track which allows
identification of the library of origin of a clone within
the mixture. The subtracted library (UI-R-C2) was
constructed as follows: PCR amplified cDNA inserts from
UI-R-C1 clones from which 3' ESTs had been derived was
used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UI-R-C2 library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996)."
BASE COUNT 86 a 133 c 117 g 128 t
ORIGIN

Query Match 19.1%; Score 318.8; DB 41; Length 464;
Best Local Similarity 86.9%; Pred. No. 9.1e-52;
Matches 403; Conservative 0; Mismatches 42; Indels 19; Gaps 4;

Qy 1208 agctcgggcccggtgcggcgagctcaagcagttcctcggtggctcaagaagcacgca 1267
|||||
Db 463 AGCTGGGGCCCGTGGGGCGCGAGCTCAGCAGTTCCTCGGCTGGCTCAAGAGCACGCG 404
|||||

Qy 1268 tactgtcgaaaccttagttccgcctgtacgaccagtggcgctgttgatgcagaagtca 1327
|||||
Db 403 TACTGTCTGAACCTTAGTTCGCGCTGTACGACAGTGGCGTCTTGGATGCAGAAAGTCA 344
|||||

Qy 1328 cacagaccggaaccagcagagggatccttcctgggcagcgggtgcggcgaga 1387
|||||
Db 343 CACAAGACCCGAACACGAGGAGGGATCCTTCCTCGGCGACGCGGGGTGCGGCGAGA 284
|||||

Qy 1398 ggtcctccggttaaaactctaagatagggccatcctcctcgtcgtt-cagacctggaggc 1446
|||||
Db 293 GGTCTCTCGCGCTAAACTCTGAGGATAGGCCATCCTCTGCTGATCGAGACCTGGAGGC 224
|||||

Qy 1447 tcacctgaattggagccctcctctgtac-----catctgggcaacaagaaacctaccagag 1501
|||||
Db 223 TCACCTGAACCTGGAGACCATCTGTACTGTCTACTTTGGGGCAATGAAGAAACCAACAGGG 164
|||||

Qy 1502 gctggggcacaatagctcccaacacacagcttctgtccacatgattggtcacacttggga 1561
|||||
Db 163 GCTGGGGCACAATAGCTCCCAACCAACACAGCTTTGG-CCACATGATGGTCACACTTTGGA 105
|||||

Qy 1562 tataccocagtggtggtaaggttg-----gggtattgcagggcctcccaacaa 1609
|||||
Db 104 TGTACCCCAATATGGGTAGGTTGGAGTATGACAAGGGTTATCGAGGACCTCTCAAGAG 45
|||||

Qy 1610 tctctttaataataaaggaggtgttcaggtataaaaaa 1653
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Db 44 TCTCTTGAATAATAGAAAGAGTTAAAAA 1

Search completed: September 28, 1999, 15:38:09
Job time: 3277 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 28, 1999, 16:39:10 ; Search time 3489.95 Seconds
(without alignments)
854.777 Million cell updates/sec

Title: US-09-037-657-16

Perfect score: 938

Sequence: 1 ggcaccgtttactctgtcca.....aaaaaaaaaaaaaaaaaaaaa 938

Scoring table: IDENTITY_NUC

Searched: 679419 seqs, 1590154680 residues

Database: GenEmbl.*

- 1: gb_ba1.*
- 2: gb_ba2.*
- 3: gb_em.*
- 4: gb_ov.*
- 5: gb_pat.*
- 6: gb_ph.*
- 7: gb_pl1.*
- 8: gb_pl2.*
- 9: gb_pr1.*
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- 11: gb_pr3.*
- 12: gb_ro.*
- 13: gb_st.*
- 14: gb_sts.*
- 15: gb_sy.*
- 16: gb_un.*
- 17: gb_vi.*
- 18: em_fun.*
- 19: em_htg.*
- 20: em_hum1.*
- 21: em_hum2.*
- 22: em_in.*
- 23: em_om.*
- 24: em_or.*
- 25: em_ov.*
- 26: em_pat.*
- 27: em_ph.*
- 28: em_pl.*
- 29: em_ro.*
- 30: em_sts.*
- 31: em_sy.*
- 32: em_un.*
- 33: em_vi.*
- 34: gb_htg1.*
- 35: gb_htg2.*
- 36: gb_in1.*
- 37: gb_in2.*
- 38: em_ba1.*
- 39: em_ba2.*
- 40: em_hum3.*
- 41: em_hum4.*
- 42: gb_pr4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	938	100.0	938 5 A70386	A70386 Sequence 16

2	888	94.7	1930	5	A70392
3	738.8	78.8	6663	5	A70398
4	738.8	78.8	11832	5	A70408
5	305	32.5	1629	5	A70382
6	304	32.4	1673	5	A70384
7	249.8	26.6	1391	5	A70394
8	249.6	26.6	1716	11	AF039293
9	218	23.2	4668	11	AC003112
10	71.2	7.6	1528	17	PEAVGAT
11	67	7.1	1319	10	HSVHTPE
12	66.2	7.1	1934	5	A49139
13	66	7.0	834	5	A70388
14	65.6	7.0	2394	11	AF031795
15	65.6	7.0	2472	4	AF151685
16	65.2	7.0	1559	4	OLJ000937
17	64.4	6.9	1013	12	RN075932
18	64.2	6.8	2180	42	AF106697
19	64	6.8	10660	10	HSSCA1
20	64	6.8	2755	12	S83440
21	63.6	6.8	1373	10	HSY14040
22	63.6	6.8	1104	37	AF047611
23	63.4	6.8	3820	5	E02221
24	63.4	6.8	3581	5	E07381
25	63.4	6.8	3271	7	FSU51671
26	63.4	6.8	1845	10	HSM800467
27	63.2	6.7	5173	5	I68732
28	63.2	6.7	5173	11	HSU38847
29	62.8	6.7	2055	7	TAU48227
30	62.6	6.7	2628	5	I66342
31	62.6	6.7	1577	7	OSCHSLKCN
32	62.6	6.7	4358	12	AF032686
33	62.6	6.7	1981	36	AFACHA
34	62.2	6.6	394	15	SYNHET505
35	62	6.6	1032	3	AF013214
36	62	6.6	907	8	ATU95035
37	61.8	6.6	2300	10	HSXR7MR
38	61.8	6.6	6330	12	MMU49908
39	61.6	6.6	1394	5	A07588
40	61.6	6.6	2245	7	ATY17053
41	61.6	6.6	541	7	SHY16247
42	61.6	6.6	3500	11	AF038440
43	61.6	6.6	2814	11	HSU73682
44	61.6	6.6	1315	12	AF082526
45	61.6	6.6	1591	12	AF087943

ALIGNMENTS

RESULT 1	A70386	A70386	938 bp	DNA	PAT	07-MAY-1999
LOCUS	Sequence 16	from Patent WO9811225.				
DEFINITION	A70386					
ACCESSION	94774665					
NID	A70386.1	GI:4774665				
VERSION	unidentified.					
KEYWORDS	unclassified.					
SOURCE	unclassified.					
ORGANISM	1 (bases 1 to 938)					
REFERENCE	Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S., Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and Kikuchi, Y.					
AUTHORS	A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME					
TITLE	Patent: WO 9811225-A 19-MAR-1998;					
JOURNAL	NICOLA NICOS ANTONY (AU)					
FEATURES	Location/Qualifiers					
source	1..938					
	/organism="unidentified"					
	/db_xref="taxon:32644"					
CDS	<1..468					
	/note="unnamed protein product"					

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/codon_start=1
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/db_xref="PID:e1433693"
/db_xref="PID:g4774666"
/db_xref="GI:4774666"
/translation="GTVFVQVRNPFYIGSKKAGIWSHPTAASPTPSRPPGP
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GKLGACVGGKAEERDPGQPPHRTLLSKHRTGSCPRADGVVRVREGSG"
BASE COUNT      243 a   245 c   272 g   178 t
ORIGIN

      1 ggcacggttacttcgaagtggtgttaacccattcggtatctatgggtcgaaaaag 60
      2 1 GGCACCGTTTACTTCTCCAAAGTGGCTTAAACCATTCGGATCTATGGTTCGAAAAAG 60
      3 61 ggggaactggagcagtgagccaccaccgctgctccaccctcgaaagtgaagc 120
      4 61 GCGGGAATCTGAGCAGTGGAGCACCACCGCTGCCCTCCACCCCTCGAAGTGAGCGC 120
      5 121 cggggcccgggcggggtgtgagcgcgcgggcgagcgcagcagcagcagcagcgggtg 180
      6 121 CCGGGCCCGGGCGGGGTGTGCGAGCGCGGGGCGGCGAGCCAGCTCGGGCCGGTG 180
      7 181 cggcgagcgaagcagttctcggtggtgtaagaagcagcagcagcagcagcagcagc 240
      8 181 CGCGCGGAGCTAAGCAGTTCCTCGGCTGGCTCAAGAACGACGACATCTGCTGACCTT 240
      9 241 agttccgctgtacaccagtgctgtgtgagcagcagcagcagcagcagcagcagc 300
      10 241 AGTTCCGCTGTACACCACTGGCTGTGGATCGAAGTCAACAGTCAACAGACCCGAAAC 300
      11 301 cagtgagaaagtggggagggttcgtgggggttaaggagcagagagagagagagac 360
      12 301 CAGTAGGAAAGTTGGGGAGGCTTCGCTGGGGGTAAAGGACGACAGAGAGAGAGAC 360
      13 361 cgggtgagcagcctccaaacaccgactctcttccaaagcagcagcagcagcagcagc 420
      14 361 CGGGGTGAGCAGCTCCACAAACACCGACTCTCTTTTCCAAAGCAGAGACGAGGGATCC 420
      15 421 tgccttcggcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
      16 421 TGCCCTCGGGCAGACGGGGTGGCGGAGAGGTAAAGGGGTCTGGGTGAGTGGGGCTTACA 480
      17 481 gtagcttagatgagcccttccctcctcctcctcctcctcctcctcctcctcctcct 540
      18 481 GCAGCTAGTAGAGGCCCTTCCCTCCCTTCCTCGGTGTGCTCAAGGGATCTCTTAGTCT 540
      19 541 cattcaaccactgcaaaagcagcagcagcagcagcagcagcagcagcagcagcagc 600
      20 541 CATTTACCCACATGCAAGAGCCGACAGTTTACTGTCATCATCAAGTTGCTGAAGGGTCC 600
      21 601 agcttaagtgcctcttcttgcctcagctcagctcagctcagctcagctcagctcagc 660
      22 601 AGGCTTAATGTGGCCCTTTTTCGCCCTCAGGTCTCGCCGGCTAAACTCTAAGGATAGGC 660
      23 661 catctcctggtggtcagacctggagctcacctgaattggagcagcagcagcagcagc 720
      24 661 CATCTCTCTGCTGGGTGAGGCTGAGGCTCAGCTGAAATGGAGCCCCCTCTGTACCTATC 720
      25 721 tgggcaacaagaacactacatgagcgtggggcacaatgagctccacacacacagcgtt 780
      26 721 TGGCAACAAGAAGAACCTACCATGAGGCTGGGGCACAATGAGCTCCCAACACACAGCTT 780
      27 781 tgggtcacatgaggtcacactggatatatacccccagctgtgggttaagggttggtattgca 840
      28 781 TGGTCCACATGATGGTTCACACTTGGATATACCCCGAGTGGGTAAAGGTTGGGGTATTGCA 840
      29 841 gggcctcccaacaatctctttaataataaagaggtgttcagggttaaaaaaaaaa 900
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Db 841 GGGCTCCCAACAATCTCTTTAAATAATAAGGAGTGTGTTTCAGGTAAAAA 900
Qy 901 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 938
Db 901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 938

RESULT 2
A70392 1930 bp DNA PAT 07-MAY-1999
LOCUS A70392 Sequence 22 from Patent WO9811225.
DEFINITION A70392
ACCESSION 94774670
VERSION A70392.1 GI:4774670
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1930)
AUTHORS Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S.,
Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and
Kikuchi, Y.
TITLE A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
JOURNAL Patent: WO 9811225-A 19-MAR-1998;
NICOLA NICOS ANTONY (AU)
FEATURES
Source
Location/Qualifiers
1..1930
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 375 a 623 c 561 g 371 t
ORIGIN

Query Match 94.7%; Score 888; DB 5; Length 1930;
Best Local Similarity 100.0%; Pred. No. 9.1e-158;
Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggcacggttacttcgaagtggtgttaacccattcggtatctatgggtcgaaaaag 60
Db 1043 GGCACCGTTTACTTCTCCAAAGTGGCTTAAACCATTCGGATCTATGGTTCGAAAAAG 1102
Qy 61 ggggaactggagcagtgagccaccaccgctgctccaccctcgaaagtgaagc 120
Db 1103 GCGGGAATCTGAGCAGTGGAGCACCACCGCTGCCCTCCACCCCTCGAAGTGAGCGC 1162
Qy 121 cggggcccgggcggggtgtgagcgcgcgggcgagcgcagcagcagcagcagcgggtg 180
Db 1163 CCGGGCCCGGGCGGGGTGTGCGAGCGCGGGGCGGCGAGCCAGCTCGGGCCGGTG 1222
Qy 181 cggcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240
Db 1223 CGCGCGGAGCTCAACGAGTTCCTCGGCTGGCTCAAGAACGACGATCTGCTCGAACCTT 1282
Qy 241 agttccgctgtacaccagtggtggtggtggtggtggtggtggtggtggtggtggtg 300
Db 1283 AGTTCCGCTGTACACCACTGGCTGTGGATCGAAGTCAACAGTCAACAGACCCGAAAC 1342
Qy 301 caggttaggaaagtggggagggttcgtgggggttaaggagcagagagagagagagac 360
Db 1343 CAGGTAGGAAAGTTGGGGAGGCTTTCGCTGGGGGTAAAGGAGAGAGAGAGAGAGAC 1402
Qy 361 cgggtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420
Db 1403 CGGGGTGAGACGCTCCCAACACCGCACTCTCTTTCCAAAGCAGGACGAGGGGATCC 1462
Qy 421 tgccttcggcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
Db 1463 TGGCTTCGGCGAGCGGGGTGGCGGAGAGGTAAAGGGGTCTGGGTGAGTGGGGCTTACA 1522
Qy 481 gcagttatagatgagcccttccctcctcctcctcctcctcctcctcctcctcctcct 540
Db 1523 GCAGTCTAGATGAGGCCCTTTCCCTCCTCTCGGTGTGCTCAAGGGATCTCTTAGTGTCT 1582
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QY 541 catttaccactgcaagagagccaggttttactgcatcatcaagttgtgaggggtcc 600
Db 1583 CATTTCACCCACTGCAAGAGAGCCAGGTTTACTGTCATCATCAAGTTGCTGAAGGTCC 1642
QY 601 aggttaattgtggtctcttttgcctcagtgctgcgggctaaacttaaggtatagc 560
Db 1643 AGGCTTAATGTGGCTCTTTTCTGCCCTCAGTCTCGCCGCTAAACTCTAAGGATAGC 1702
QY 661 catctctctgtggtgcagacctgaggtgctacccctgaattggagccctctgtacctatc 720
Db 1703 CATCTCTCTGTGGTGCAGACCTGAGAGCTGAGGCTCACCTGAATTGGAGCCCTCTGTACTATC 1762
QY 721 tgggaacaagaacctaccattacattgaggtggtgggacaaatgagctcccaaacacagett 780
Db 1763 TGGGCAACAAGAAACCTTACCATTAGAGGTGGGGCAACAATGAGCTCCCAACACAGCTT 1822
QY 781 tgggtccacatgattgtcacacttgatatacccccagtggtggttaaggttgggtattgca 840
Db 1823 TGGTCCACATGATGTCACACTTGTGATATACCCCAAGTGTGGGTAAAGGTGGGGTATTGCA 1882
QY 841 gggctcccaacaattctttaataataaaggaggtgtttcaggtaa 888
Db 1883 GGGCTCCCAACAATCTCTTTAAATAAATAAAGGAGTGTTCAGGTAA 1930

RESULT 3
A70398
LOCUS A70398 6663 bp DNA PAT 07-MAY-1999
DEFINITION Sequence 28 from Patent WO9811225.
ACCESSION A70398
NID 94774676
VERSION A70398.1 GI:4774676
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 6663)
AUTHORS Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S., Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and Kikuchi,Y.
TITLE A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
JOURNAL Patent: WO 9811225-A 19-MAR-1998;
NICOLO NICOS ANTONY (AU)
FEATURES
source Location/Qualifiers
1. .6663
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 1462 a 1852 c 1715 g 1634 t
ORIGIN

Query Match 78.8%; Score 738.8; DB 5; Length 6663;
Best Local Similarity 96.3%; Pred. No. 8.4e-130;
Matches 778; Conservative 0; Mismatches 27; Indels 3; Gaps 2;

QY 79 tggagccaccacccgctgctccaccctcagtcgaagtgagcgcggcccgccggcgagg 138
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QY 139 gtgtgcagccggtggggtggagccagctcgggcccgtgctggtgcgagctcaagcag 198
Db 5874 GTGTGCAGCCGCGGGCGGAGCCGAGCTCGGGCCCGGTGCGCGCGGAGCTCAACGAG 5933
QY 199 ttctcgtggtggtcgaagagcagcagctactgtcgaaacctagtttccgctgtacgac 258
Db 5934 TTCTCGGCTGGCTCAAGAAGCAGCATCTGCTCGAACCTTAGTTTCCGGCTGTACGAC 5993
QY 259 cagtggcggtctgtgagtcagaaactcacaaagaccgaaacaggttaggaattgggg 318
Db 5994 CAGTGGCGGTCTGTGATGTCAGAAAGTTCACAAAGACCCGAAACACAGGTAGGAAGTTGGGG 6053
QY 319 gaggcttcgttgggggttaaaggagcagaggaagagagagaccgggtgagcagctcca 378

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Db 6054 GAGGCTTGGTGGGGGTAAAGGACACAGGAGAGAGACCCGGGTGACAGCCTCCA 6113
QY 379 caaacccgactcttcttccaaagcacagggagggggtatcctcctcgggagagggg 438
Db 6114 CAACACCCGACTCTTCTTTTCCAAGCACAGGACGAGGGGATCTGCCCCGCGGACAGCGG 6173
QY 439 gtggggcagaggttaagggtctcgtgggtgagtggtgggacctacagcagtagtagagccc 498
Db 6174 GTGGCGGCAGAGGTAAGGGGGTCTGGGTGAGTGGGGCTACAGCAGTCTAGATGAGGCC 6233
QY 499 ttteccctccttcggtgtgctcaaaaggatctcttagtctcatttaccacactgaaaa 558
Db 6234 TTTCCCTCCCTTCGGTGTGCTCAAAAGGATCTCTTAGTGTCTATTCCACCCTGCAAA 6293
QY 559 gagccccaggttttactgcatcatcaagttgctgaaggtgccaggttaattgtgctct 618
Db 6294 GAGCCCCAGGTTTACTGTCATCATCAAGTTGCTGAAGGTCACAGGCTTAATGTGCTCT 6353
QY 619 ttctgcccctcaggtcctcgcggcgtaaactcctaaagtaggagcctcctcctgctgggtca 678
Db 6354 TTTCTGCCCTCAGTCTCGCCGGCTAACTCTAAGGATAGGCCATCTCTCTGCTGGGTCA 6413
QY 679 gacctgaggtcactcgaattggagccctctgtacctatctctgggcaacaaagaaacct 738
Db 6414 GACCTGGAGGCTCACCTGAATTGGAGCCCTCTCTGAC-ATCTGGGCAACAAGAAACCT 6472
QY 739 acctgaggtcggggacaaatgagctcccaacacacagcttttggccacatgatgtca 798
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QY 799 cactgtatatacccccagtggtggttaaggttgggtattcaggggctcccaacaatctc 858
Db 6531 CACTTGGATATACCCAGTGTGGGTGGGTGGGTATTGAGGGCTTCCAGGGCTCCCAAGAGTCTC 6590
QY 859 tttaataaataaaaggaggtgttcaggt 886
Db 6591 TTTAAATAAATAAAGGAGTGTTCAGGT 6618

RESULT 4
A70408
LOCUS A70408 11832 bp DNA PAT 07-MAY-1999
DEFINITION Sequence 38 from Patent WO9811225.
ACCESSION A70408
NID 94774683
VERSION A70408.1 GI:4774683
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 11832)
AUTHORS Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S., Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and Kikuchi,Y.
TITLE A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
JOURNAL Patent: WO 9811225-A 19-MAR-1998;
NICOLO NICOS ANTONY (AU)
FEATURES
source Location/Qualifiers
1. .11832
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 2447 a 3367 c 3298 g 2720 t
ORIGIN

Query Match 78.8%; Score 738.8; DB 5; Length 11832;
Best Local Similarity 96.3%; Pred. No. 8.1e-130;
Matches 778; Conservative 0; Mismatches 27; Indels 3; Gaps 2;

QY 79 tggagccaccacccgctgctccaccctcagtcgaagtgagcgcggcccgccggcgagg 138
Db 10983 TGCGCGGCCCCCAACTGCGCTCCATTCTTTTAGAGCGCCCGCGGCCCGCGCGGG 11042

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QY	181	cggcggagctcaagcagttctcggctcggtgcgtcgaagagcagcgatcactgctgaacctt	240
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QY	241	agtttcgctgtacacacagtcgagtcggcgtgcttgatgcagaaagtcacacaaagcccgaaac	300
Db	922	AGTTCGGGCTCTACACAGCAGTGGCGAGCCTGGATGTCAGAAAGTCGCAAGACCCGCAAC	981
QY	301	cagctaggaaagtggg	317
Db	982	CAGCAGACGACGAGGGG	998
RESULT	8		
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LOCUS		1716 bp	02-AUG-1998
DEFINITION		Homo sapiens cytokine-like factor-1 precursor (CLF-1) mRNA,	
ACCESSION		AF059293	
NID		93372626	
VERSION		AF059293.1	GI:3372626
KEYWORDS			
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		1 (bases 1 to 1716)	
TITLE		Elson,G.C.A., Graber,P., Losberger,P., Herren,S., Gretener,D., Menoud,L.N., Wells,T.N.C., Kosco-Vilbois,M.H. and Gauchat,J.F.	
JOURNAL		CLF-1, a Novel Soluble Protein Shares Homology With Members of the Cytokine Type-I Receptor Family	
REFERENCE		J. Immunol. (1998) in press	
AUTHORS		2. (bases 1 to 1716)	
TITLE		Elson,G.C.A., Graber,P., Losberger,P., Herren,S., Gretener,D., Menoud,L.N., Wells,T.N.C., Kosco-Vilbois,M.H. and Gauchat,J.F.	
JOURNAL		Direct Submission	
REFERENCE		Submitted (14-APR-1998) Dept. of Immunology, Serozo Pharmaceutical Research Institute, 14, Chemin des Aulx, Plan-les-Ouates, GE 1228, Switzerland	
FEATURES		Location/Qualifiers	
source		1. .1716	
gene		/organism="Homo sapiens"	
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		1. .1716	
		/gene="CLF-1"	
		119. 1387	
		/gene="CLF-1"	
		/note="similar to cytokine type-1 receptor family members; similar to the sequence presented in GenBank Accession Number AC003112"	
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		/product="cytokine-like factor-1 precursor"	
		/protein_id="AAC28335.1"	
		/db_xref="PID:93372627"	
		/db_xref="GI:3372627"	
		/translation="MPAGRRGPAQASARRPPPLLLLLCVLGAPRAGSGATVATIS PDPTLLIGSSLLATCSVHGPPPGATAGSLVYTLNRRLPPELSRVNASTLALALALNGSRORSQDNLVCHARGSDILAGSLVGLPPEKPNVCSKWNKMDLTCRTTPGNGTETFLTNYSLYKLRWQDNTCEIYHTVGHSPHCPKIDALFTPEYVEATNRIGSARSDVLTLIDVYTTDPPDHVSRVGGLEDLSVRWVSPPAKDFLQAKYQIRYRVSDVDMKVDVSNQTSCLAGLKGPTVYFVQVRCNPFGLYSGKAGKAWSEWSPYAASTPRSERPGGACPRGPESSGPRVRELAQLGLWLLKKHAYCSNLSFRLYDWRANWQKSHKTRNQGEGILPSGRRGTARGPAR"	
		119. 229	
sig_peptide		/gene="CLF-1"	
		/note="putative"	
		230. .1384	
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		/note="putative"	
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BASE COUNT      295 a      623 c      525 g      273 t
ORIGIN

Query Match      26.6%; Score 249.6; DB 11; Length 1716;
Best Local Similarity 88.8%; Pred. No. 6.2e-38;
Matches 270; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 ggcaccgtttacttcgtccaaagtctgttaaccattcggaatctatgggtcgaagaag 60
Db 1028 GGCACCGTGTACTTCGTCGAAGTGGCTGCAACCCCTTGGCACTATGGCTCCAGAAA 1087

Qy 61 gcgggaactctgagcgagtgagccacccaccgctgctccaccctcgaagtgcgc 120
Db 1088 GCCGGATCTGGAGTGAAGTGGAGCCACCCACAGCCGCTCCATCCCGAGTGAGCGC 1147

Qy 121 ccgggcccggcggggggtgtgagccgcgggcgggcgccagctcgggcccgggtg 180
Db 1148 CCGGCGCGGGCGGGCGGGCGTGGCAACCGGGCGGAGAGCGAGTCCGGGGCCGGTG 1207

Qy 181 cggcgagctcaagcagcttctcggctggtcgaagagcgcacatactctcgaacctt 240
Db 1208 CGCGCGAGCTCAAGCAGTCTCTTGGCTGGCTCAAGAAGCAGCGTACTGTCTCAACCTC 1267

Qy 241 agtttccgctgtacgaccagtggtgtgtgttgatgcagaagtcacacaagaccgaaac 300
Db 1268 AGCTTCGCCCTTACGACCAGTGGCGAGCGCTGGATGCAGAGTGCACACAGCCGCAAC 1327

Qy 301 cagg 304
Db 1328 CAGG 1331

RESULT 9
AC003112/c AC003112 40668 bp DNA PRI 21-NOV-1997
LOCUS Human DNA from chromosome 19 specific cosmid R30292, genomic
DEFINITION sequence, complete sequence.
ACCESSION AC003112
NID 92836669
VERSION AC003112.1 GI:26366669
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 40668)
AUTHORS Lamerdin,J.E., McCready,P.M., Adamson,A.W., Burkhardt-Schultz,K.,
Gordon,L., Christensen,M., Kyle,A., Ramirez,M., Stilwagen,S.,
Garnes,J., Danganan,L., Bruce,R., Quan,G., Montgomery,M., Ow,D.,
Kobayashi,A., Olsen,A.O. and Carrano,A.V.
TITLE Sequence analysis of an ~1 Mb region containing the MEF2B gene in
19p12
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 40668)
AUTHORS Lamerdin,J.E.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-1997) Human Genome Center, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
FEATURES
source
1. .40668
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/db_xref="taxon:9606"
/clone="R30292"
/chromosome="19"
/map="19p12 between UBA52 and D19S451"
/clone_lib="LL19NC03 R chromosome 19 cosmid library"
/note="LL19NC03 cosmid library constructed at LLNL from
flow-sorted chromosomes from hybrid 5HL2-B, which carries
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complement(6..62)
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misc_feature

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misc_feature complement(1383..1444)
/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: good, score: 62.000"
LTR 2257..8516
/standard_name="endogenous retroviral sequence"
/note="HBV9 retroviral sequence"
complement(3269..3544)
/rpt_family="Alu"
5425..5722
/rpt_family="Alu"
complement(6486..6772)
/rpt_family="Alu"
complement(7505..7783)
/rpt_family="Alu"
8951..9254
/rpt_family="Alu"
9358..9535
/rpt_family="LTR12"
complement(9445..9505)
/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: good, score: 63.000"
misc_feature complement(9629..9672)
/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 75.000"
repeat_region complement(9928..10123)
/rpt_family="Alu"
10409..10548
/note="DSS similarity to AA047548 zf15e02.r1 Soares fetal
heart NBHH19W Homo sapiens cDNA clone 377018 5' (1..138);
96% identity.--Other overlapping matches:-(10435..10548)
DSS similarity to AA136115 zk90b04.r1 Soares pregnant
uterus NBHPU Homo sapiens cDNA clone 490063 5' (1..110);
93% identity.--(10466..10548) DSS similarity to AA432628
zx33f04.r1 Soares total fetus NB2HF8 9w Homo sapiens cDNA
clone 788287 5' (1..82); 95% identity.--(10486..10548) DSS
similarity to AA009412 ze82h02.r1 Soares fetal heart
NBHH19W Homo sapiens cDNA clone 365523 5' (1..61); 97%
identity."
10843..10725
/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 100.000--DSS
similarity to AA047548 zf15e02.r1 Soares fetal heart
NBHH19W Homo sapiens cDNA clone 377018 5' (139..221); 100%
identity.--DSS similarity to AA136115 zk90b04.r1 Soares
pregnant uterus NBHPU Homo sapiens cDNA clone 490063 5'
(111..192); 99% identity.--DSS similarity to AA432628
zx33f04.r1 Soares total fetus NB2HF8 9w Homo sapiens cDNA
clone 788287 5' (83..165); 100% identity.--DSS similarity
to AA009412 ze82h02.r1 Soares fetal heart NBHH19W Homo
sapiens cDNA clone 365523 5' (62..144); 100% identity."
11127..11331
/note="DSS similarity to AA136115 zk90b04.r1 Soares
pregnant uterus NBHPU Homo sapiens cDNA clone 490063 5'
(193..394); 94% identity.--DSS similarity to AA009412
ze82h02.r1 Soares fetal heart NBHH19W Homo sapiens cDNA
clone 365523 5' (145..346); 96% identity.--(1121..1131)
DSS similarity to AA009693 ze82h02.s1 Soares fetal heart
NBHH19W Homo sapiens cDNA clone 365523 3' (429..307); 95%
identity.--(11127..11246) DSS similarity to AA047548
zf15e02.r1 Soares fetal heart NBHH19W Homo sapiens cDNA
clone 377018 5' (222..341); 97% identity.--(11061..1131)
predicted exon, program: grail2exons_human_1.3, frame: 0,
quality: good, score: 73.000--(11061..11209) DSS
similarity to AA452628 zx33f04.r1 Soares total fetus
NB2HF8 9w Homo sapiens cDNA clone 788287 5' (167..313);
98% identity."
complement(11869..12161)
/rpt_family="Alu"
12502..12581
/note="DSS similarity to AA136115 zk90b04.r1 Soares

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pregnant uterus NbHPU Homo sapiens cDNA clone 490063 5'
(395..477); 92% identity.--DSS similarity to AA009412
ze82h02.r1 Soares fetal heart NBH19W Homo sapiens cDNA
clone 36523 5' (347..427); 94% identity.--DSS similarity
to AA009693 ze82h02.s1 Soares fetal heart NBH19W Homo
sapiens cDNA clone 36523 3' (306..228); 99%
identity.--DSS similarity to AA450010 zc33f04.s1 Soares
total fetus Nb2HF8 9w Homo sapiens cDNA clone 788287 3'
(309..229); 94% identity.--
complement(12966..13240)
/rpt_family="Alu"
/rpt_family="Alu"
complement(13274..13531)
/rpt_family="Alu"
complement(13756..14029)
/Note="Predicted exon, program: grill2exons_human_1.3,
frame: 2, quality: good, score: 61.000--Other overlapping
matches:-(13756..13826) DSS similarity to AA009412
ze82h02.r1 Soares fetal heart NBH19W Homo sapiens cDNA
clone 36523 5' (428..496); 97% identity.--(13756..13984)
DSS similarity to AA009693 ze82h02.s1 Soares fetal heart
NBH19W Homo sapiens cDNA clone 36523 3' (227..1); 98%
identity.--(13756..13984) DSS similarity to AA450010
zc33f04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
clone 788287 3' (228..1); 99% identity.--
complement(14100..14672)
/rpt_family="Alu"
1485..15317
/Note="DSS similarity to AA046406 zville07.s1 Soares NbHMPu
S1 Homo sapiens cDNA clone 753348 3' (1..433); Score: 858
Identity: 431/433 (99%);--(14884..15237) DSS similarity
to W3175 zb2la02.r1 Soares fetal lung NBH19W Homo
sapiens cDNA clone 302666 5' (1..355); 94%
identity.--(15227..14885) DSS similarity to AA121532
zk89c11.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA
clone 490004 3' (342..1); 99% identity.--(15227..14885)
DSS similarity to AA127694 zk89c11.r1 Soares pregnant
uterus NbHPU Homo sapiens cDNA clone 490004 5' (126..467);
99% identity.--(15227..14897) DSS similarity to W46603
zc32h10.r1 Soares senescent fibroblasts NbHSF Homo sapiens
cDNA clone 324067 5' (328..1); 98%
identity.--(15227..15088) DSS similarity to W46604
zc32h10.s1 Soares senescent fibroblasts NbHSF Homo sapiens
cDNA clone 324067 3' (322..465); 96% identity.--
15713..15760
/Note="DSS similarity to AA121532 zk89c11.s1 Soares
pregnant uterus NbHPU Homo sapiens cDNA clone 490004 3'
(383..343); 99% identity.--DSS similarity to AA127694
zk89c11.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA
clone 490004 5' (77..125); 90% identity.--(15735..15713)
DSS similarity to W46603 zc32h10.r1 Soares senescent
fibroblasts NbHSF Homo sapiens cDNA clone 324067 5'
(351..329); 100% identity.--(15735..15713) DSS similarity
to W46604 zc32h10.s1 Soares senescent fibroblasts NbHSF
Homo sapiens cDNA clone 324067 3' (299..321); 100%
identity.--
complement(15895..16082)
/Note="Predicted exon, program: grill2exons_human_1.3,
frame: 0, quality: excellent, score: 81.000--Other
overlapping matches:-(15936..15895) DSS similarity to
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sapiens cDNA clone 490004 3' (431..390); 100%
identity.--(15970..15895) DSS similarity to AA127694
zk89c11.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA
clone 490004 5' (1..76); 100% identity.--
17926..18190
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complement(18270..18438)
/Note="Predicted exon, program: grill2exons_human_1.3,
frame: 0, quality: excellent, score:
100.000--(18438..18284) DSS similarity to W66776
me17b11.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus
cDNA clone 387741 5' similar to FIR:B38252 B38252
granulocyte colony-stimulating factor precursor

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(157..1); 82% identity.--(18438..18406) DSS similarity to
AA049280 mj45d02.r1 Soares mouse embryo NBME13.5 14.5 Mus
musculus cDNA clone 479043 5' similar to SW:IL6_MOUSE
Q00560 INTERLEUKIN-6 RECEPTOR BETA PRECURSOR (432..464);
88% identity.--
complement(18540..18697)
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frame: 1, quality: excellent, score: 100.000--DSS
similarity to W66776 me17b11.r1 Soares mouse embryo
NBME13.5 14.5 Mus musculus cDNA clone 387741 5' similar to
FIR:B38252 B38252 granulocyte colony-stimulating factor
receptor precursor (316..158); 92% identity.--DSS
similarity to AA049280 mj45d02.r1 Soares mouse embryo
NBME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to
SW:IL6_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN
PRECURSOR (274..431); 93% identity.--"

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misc_feature

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Query Match      23.2%; Score 218; DB 11; Length 40668;
Best Local Similarity 72.4%; Pred. No. 4.3e-32;
Matches 314; Conservative 0; Mismatches 85; Indels 35; Gaps 1;

QY 105 cctcgaagtgaagccgcccggcgggggtgtcgcagccgcccggcgagcgc 164
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Db 16093 CCACACACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGCC 16034

QY 165 caqctcggcgccggtgcgcgagctcaagcagcttcctcgctcgaagaagcagcgc 224
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Db 16033 GAGCTCGGGCGCGGTGCGCGCGCGAGCTCAAGCAGTCTCTGGCTCAAGAGCAGCGC 15974

QY 225 atactgtctgaaccttagttccgcctctacgaccagtcgctgttgcgttcgagcagc 284
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Db 15973 GFACGTGCTCAACCTCAGCTCCCGCTCTAGACAGTGGCGAGCTGGATGCAGAAATC 15914

QY 285 acacaagcccgaaaccaggttagaagaa 313
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Db 15913 CCACAAGACCGCGCAACCAAGTAGGAAGAGGAGGAGCGCTCGCGGTGGGGTGACAGGG 15854

QY 313 ---ttgggggaggttcgttgggggtaaaagagcagagagagagagaccgggtgag 369
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 15853 AGCTGGGGGGGCCCGAGAAAACAGGGGAGGGAGAGACAGCAGAGCTGTGGAGCAGCTGTG 15794

QY 370 cagctccacacacgcgcactcttcttccaaagcacagcagagagagagagctcctgcctcg 429
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 15793 CAGCCCCCAGCAGACCTCTGCTTCTTCCAAAGCAGAGCAGAGGAGGATCTCTGCCCTCGG 15734

QY 430 gcagacgggttcgctgcgagaggttaagggggtctgggtgagtggggctcagcagctag 489
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 15733 GCAGCGGGGCGCAGCGAGAGGTAAAGTGGGCGCTGAATGGTGGCGGGGAGGAGCAAGG 15674

QY 490 atgagggcctttcc 503
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Db 15673 GGAGGGCCCCCTTC 15660

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RESULT 10

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PEAVGEN      PEAVGEN      15528 bp      mRNA      VRL      29-JAN-1998
LOCUS        Plasmid PEAY030 containing cDNA of Equine arteritis virus, complete
DEFINITION   genome.
ACCESSION    Y07862
NID          Y07862
VERSION      Y07862.1
KEYWORDS     GI:1835169
              Gl gene; glycoprotein; Gs gene; membrane protein; nucleocapsid
              protein; ORF1a; ORF1ab; ORF3; ORF4; replicase; replicase
              polyprotein; ribosomal frameshift signal.
SOURCE       Equine arteritis virus.
ORGANISM     Equine arteritis virus.
              Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
              Arteriviridae; Arterivirus.
REFERENCE    1 (bases 1 to 15528)
AUTHORS      van Dinten,L.C., den Boon,J.A., Wassenaar,A.L., Spaan,W.J. and
              Snijder,E.J.
TITLE        An infectious arterivirus cDNA clone: identification of a replicase

```

point mutation that abolishes discontinuous mRNA transcription
 Proc. Natl. Acad. Sci. U.S.A. 94 (3), 991-996 (1997)
 9715715
 2 (bases 1 to 15528)
 Snijder E.J.
 Direct Submission
 Submitted (10-SEP-1996) E.J. Snijder, Dept. of Virology, Institute
 of Medical Microbiology, Leiden University, AZL Building 1, Room
 P4-26, Postbus 9600, 2300 RC Leiden, NETHERLANDS
 Related sequences: X53459, X52275, X52276, X52277 & A02710.
 Location/Qualifiers
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 /db_xref="taxon:57026"
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 HMRGSPORAWHITTRSCKLKYYVCDISEADWCLPAGNYGYPGPGAGYRCILA
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 PRVPAPRVSANSQDVDPAPVPPKRTKLANPTQAPIPAPRLOGASTQ
 EPLASAGVSDAPKRWAKTVISSAERFTELVRQSRVGVQDVLUQALPKTPAVQRI
 TMTLKMRSFQSWCVDWYVPLAVIACLLIPWLSALLSFAIGLIPVGNVYVLTALL
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 LYNRTASGVDPALLRVGQDFLKNPGRFLIGWYIGICYFVLVYVSTFCLPIKCG
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 AAAPTNSLLGVARDCVYTGTTTLYIPKEGMVFEGLRSPKARGNVGTVAGSSYGTGS
 VMTNRNEVVYLTASHVVRANMATLKGDMATLTFFKNGDFAEAVTITSELPGNMPQ
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 5399..5405
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 9824..10507
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CDS

misc_feature

gene

CDS

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gene      11146..11913
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CDS      11901..12369
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Best Local Similarity 71.1%; Pred. No. 0.00016;
Matches 108; Conservative 0; Mismatches 43; Indels 1; Gaps 1;
QY 788 catgatggtcacacttgatatacccccagtggtg-gtaaggtggggattgtagggcct 846
Db 12635 CAGGCGCGTAAGACGTGGATATCTCTGTGTGCGTCATGTTGAAGTAGTTATTAGCCA 12694
QY 847 cccaacaatctctttaaataaataaggaggttcttcagggtataaataaataaataa 906
Db 12695 CCACGAGACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 12754
QY 907 aaaaaaataaataaataaataaataaataa 938
Db 12755 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 12786
RESULT 11
HSVHATPE      1319 bp      mRNA      PRI      01-FEB-1994
LOCUS      H.sapiens mRNA for vacuolar H+ ATPase E subunit.
DEFINITION      X76228
ACCESSION      X76228
NID      9452657
VERSION      X76228.1 GI:452657
KEYWORDS      ATPase epsilon subunit; vacuolar H+ ATPase E subunit.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 1319)
AUTHORS      Lipinski, M.
TITLE      Direct Submission
JOURNAL      Submitted (02-NOV-1993) M. Lipinski, Lab. de Biologie des Tumeurs
Humaines, CNRS URA 1156, Inst. Gustave Roussy, 94805 Villeuif
Cedex, FRANCE

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REFERENCE      2 (bases 1 to 1319)
AUTHORS      Baud, V., Mears, A.J., Lamour, V., Scamps, C., Duncan, A.M.,
McDermid, H.E. and Lipinski, M.
TITLE      The E subunit of vacuolar H(+) ATPase localizes close to the
centromere on human chromosome 22
JOURNAL      Hum. Mol. Genet. 3 (2), 335-339 (1994)
MEDLINE      94272476
FEATURES
SOURCE      Location/Qualifiers
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POLYA_signal      1243..1248
BASE COUNT      415 a 279 c 303 g 322 t
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Query Match      7.1%; Score 67; DB 10; Length 1319;
Best Local Similarity 83.5%; Pred. No. 0.0012;
Matches 76; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 848 ccaacaatctctttaaataaataaggaggttcttcagggtataaataaataaataa 907
Db 1224 CCATGAATGCTTTATTTATTAAGAGCTTATCGGNAAAAAAAAAAAAAAAAAA 1283
QY 908 aaaaaaataaataaataaataaataaataa 938
Db 1284 AAAAAAAAAAAAAAAAAAAAAAAAAA 1314
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A49139      1934 bp      DNA      PAT      07-MAR-1997
LOCUS      Sequence 1 from Patent WO9605300.
DEFINITION      A49139
ACCESSION      A49139
NID      92302694
VERSION      A49139.1 GI:2302694
KEYWORDS
SOURCE      Norway rat.
ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE      1 (bases 1 to 1934)
AUTHORS      Enmark, E. and Gustafsson, J.A.
TITLE      OR-1 ON ORPHAN RECEPTOR BELONGING TO THE NUCLEAR RECEPTOR FAMILY
JOURNAL      Patent: WO 9605300-A 1 22-FEB-1996;
KAROBIO AB (SE)
COMMENT      Other publication AU 3384495 960307.
FEATURES
SOURCE      Location/Qualifiers
1..1934
/organism="Rattus norvegicus"
/strain="SPRAGUE DAWLEY"
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BASE COUNT      440 a 588 c 544 g 362 t
ORIGIN

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Query Match 7.1%; Score 66.2; DB 5; Length 1934;
Best Local Similarity 74.8%; Pred. No. 0.0016;
Matches 83; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 827 gttggggtattcagggcccccacacatctcttaataataaaggagggtgttcaggt 886
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Db 1824 GTTGGGAGACACAGGCCCTCTTCTGCCCTTTATTATATAAATAAATAA 1883
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QY 887 aa 937
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Db 1884 AA 1934
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RESULT 13
A70388 834 bp DNA PAT 07-MAY-1999
DEFINITION Sequence 18 from Patent WO9811225.
ACCESSION A70388
NID 94774667
VERSION A70388.1 GI:4774667
KEYWORDS
SOURCE
ORGANISM
unidentified.
unidentified.
unclassified.
REFERENCE 1 (bases 1 to 834)
AUTHORS Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S., Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and Kikuchi, Y.
TITLE A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
JOURNAL Patent: WO 9811225-A 19-MAR-1998;
NID NICOLA NICOS ANTONY (AU)
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BASE COUNT 167 a 274 c 225 g 168 t

Query Match 7.0%; Score 66; DB 5; Length 834;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggcacgttactctcgaagtcgctgttaaccattcggtatcattggtcgaaag 60
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Db 769 GGCACGTTTACTCTGTCGACGCGCTGTGACCCATTCCGGATCTATGGGTCGAAAG 828
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QY 61 gcggga 66
|||||
Db 829 GCGGA 834
|||||

RESULT 14
AF061795 2394 bp mRNA PRI 12-SEP-1998
LOCUS Homo sapiens dynamin-like protein DYNIV-11 (DYNIV-11) mRNA, complete cds.
DEFINITION
ACCESSION AF061795
NID AF061795 93126873

AF061795.1 GI:3126873
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2394)
AUTHORS Hong, Y.R., Chen, C.H., Cheng, D.S., Howng, S.L. and Chow, C.C.
TITLE Human dynamin-like protein interacts with the glycogen synthase kinase 3 beta
JOURNAL Biochem. Biophys. Res. Commun. 249 (3), 697-703 (1998)
MEDLINE 98401153
REFERENCE 2 (bases 1 to 2394)
AUTHORS Hong, Y.R., Chen, C.H., Cheng, D.S. and Chou, C.K.
TITLE Direct Submission
JOURNAL Submitted (28-APR-1998) Graduate Institute of Biochemistry, No.100, Shih-Chuan 1st Road, Kaohsiung, Taiwan, ROC 80708, Taiwan, ROC
FEATURES
source
1. .2394
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="liver"
/dev_stage="fetus"
22..2121
/note="large G-protein; dyn IV; expressed in heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas; 37 amino acid in frame deletion"
/codon_start=1
/product="dynamin-like protein Dymple isoform"
/protein_id="AAC35283.1"
/db_xref="PID:g3126874"
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LMDAGTDAMDVLMGRVFPVKLGIIIVNRSQDINNKKSVDSIRDEYAFQKYPSSL
ANRNGTYLARTNLRLMHHRIDCLPELKTINVAQYQLLSNSYGPDPKSAITLL
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TQELLRPKLDHDAIVEVYVTCLLRRLPVNEMVNLVAELAYINTKHPDFAACGLM
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LQASQIIAIEIRETHLW"

BASE COUNT 810 a 444 c 521 g 619 t

Query Match 7.0%; Score 65.6; DB 11; Length 2394;
Best Local Similarity 76.9%; Pred. No. 0.0021;
Matches 80; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 835 attgcagggtccccaacaatctttaaataataaaggagggtgttcaggtaaaaaa 894
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Db 2272 ATTGCAGAACACATCACACATTAAATCCAAATAATAATGCTGTTCAAAAAA 2331
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QY 895 aa 938
|||||
Db 2332 AA 2375
|||||

RESULT 15
AF151685 2472 bp mRNA PRI 17-JUN-1999
LOCUS Homo sapiens dynamin-like protein DYNIV-11 (DYNIV-11) mRNA, alternatively spliced, complete cds.
DEFINITION
ACCESSION AF151685
NID 95081793
VERSION AF151685.1 GI:5081793
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

Search completed: September 28, 1999, 16:39:42
Job time: 6969 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 28, 1999, 16:45:17 ; Search time 303.81 Seconds
(without alignments)
772.457 Million cell updates/sec

Title: US-09-037-657-16

Perfect score: 938
Sequence: 1 99caccgttactctgtcca.....aaaaaaaaaaaaaaaaaaaaa 938

Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	938	100.0	938	1	V27142 Novel haemopoietin
2	888	94.7	1930	1	V27158 Unspliced murine N
3	738.8	78.8	11832	1	V27148 Nucleotide sequenc
4	738.8	78.8	6663	1	V27145 Nucleotide sequenc
5	305	32.5	1629	1	V27140 Novel haemopoietin
6	304	32.4	1673	1	V27141 Novel haemopoietin
7	304	32.4	1656	1	V41688 Nucleotide sequenc
8	297.6	31.7	1724	1	V70896 CDNA encoding rat
9	249.8	26.6	1391	1	V27144 Nucleotide sequenc
10	249.8	26.6	1813	1	V70895 CDNA encoding an a
11	249.6	26.6	1579	1	V41689 Nucleotide sequenc
12	249.6	26.6	1690	1	V70894 CDNA encoding huma
13	92.8	9.9	259	1	V70897 Expressed sequence
14	71.2	7.6	12827	1	V09036 Equine arteritis v
15	71.2	7.6	15528	1	V09039 Equine arteritis v
16	66.8	7.1	1711	1	V43617 Human secreted pro
17	66.2	7.1	1934	1	T13229 OR-1 orphan recept
18	66	7.0	834	1	V27143 Nucleotide sequenc
19	65	6.9	1776	1	T91744 Tobacco calcium/ca
20	64.6	6.9	742	1	V00437 Clone H905.107. Is
21	64.4	6.9	5668	1	X27262 prostate-tumour de
22	64.4	6.9	3848	1	X27277 prostate-tumour de
23	63.6	6.8	1373	1	V52969 Human GI protein i
24	63.4	6.8	3820	1	Q03517 Plasmid pGH1 enco
25	63.4	6.8	3581	1	Q44391 Sequence of murine
26	63.2	6.7	5173	1	T89783 Human immunodefici
27	63.2	6.7	819	1	V63198 CDNA from clone ga
28	63	6.7	1521	1	V73000 Human foetal brain
29	62.8	6.7	2239	1	V01527 Wheat soluble star
30	62.6	6.7	2628	1	V01060 Human PKR gene. Sc
31	62.6	6.7	4358	1	V42653 Nucleotide sequenc
32	62.6	6.7	3076	1	V73003 Human adult brain
33	62.4	6.7	1453	1	Q50573 Asparaginylendopep
34	62.4	6.7	1640	1	Q50575 Asparaginylendopep
35	62.4	6.7	1910	1	Q30579 Asparaginylendopep
36	62.2	6.6	4456	1	V81748 Human ALP encoding
37	61.6	6.6	1394	1	Q05879 Placenta-specific
38	61.6	6.6	270	1	T89602 Hepatitis C virus
39	61.6	6.6	1733	1	V81394 Human tumour antiq
40	61.4	6.5	1558	1	X22942 Human cathepsin Y
41	61.2	6.5	2339	1	Q63892 Tomato acid invert
42	61.2	6.5	2339	1	T01339 Tomato acid invert
43	61	6.5	2400	1	Q05055 Placenta-specific

44 61 6.5 3238 1 Q83532 Sequence encoding
45 61 6.5 1700 1 V11858 Mus musculus Tub I

ALIGNMENTS

```
RESULT 1
V27142
ID V27142 standard; DNA: 938 BP.
AC V27142;
DT 29-SEP-1998 (first entry)
DE Novel haemopoietin receptor NR6.3 gene.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening; ss;
KW Mouse.
OS Mus sp.
FH Key
FT CDS
FT FT
FT /tag= a
FT /product= "Haemopoietin receptor NR6.3"
W09811225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIE/) DZIEGLEWSKA H E.
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maseda M, Nash A, Nicola NA, Rakar S, Willson T,
PI Zhang J;
DR WPI; 98-260970/23.
DR P-PSDB; W55013.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PS Claim 6; Page 90-92; 182pp; English.
CC The haemopoietin receptor (HR) NR6.3 is a form of the novel HR NR6.
CC Interaction between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and its
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SQ Sequence 938 BP; 243 A; 245 C; 272 G; 178 T;
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Best Local Similarity 100.0%; Pred. No. 9.9e-170;
Matches 938; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 99caccgttactctgtccaagtgcgtgttaaccattcgggtatctatgggtcgaaaaa 60
Db 1 GSCACCGTTACTTCTGTCAGTCCAGTGGTGTGAACCCATTGCGGATCTATGGTTCGAAAAG 60
QY 61 9cgggaactctgagcagtgagcaccacccaccgtgctccaccctcgaagtgcgc 120
Db 61 GCGGGAATCTGGAGCGAGTGGAGCCACCCACCCCGTCCCTCCAGTTCGAGTGAGCGC 120
QY 121 ccgggcccggcggggggtgtgagccgcggggcgagccagctcgggccgggtg 180
Db 121 CCGGGCCCGGGCGGGGGTGTGAGCCGGGGCGGCGAGCCAGCTCGGGCCGGTG 180
QY 181 cggcgcgagctcaagcagcttctcggtcggtcgaagcagcagcagctgctcgaacctt 240
Db 181 CGGCGCGAGCTCAGCAGTTCCTCGGTGGCTCAAGAGACAGCATACTGCTCGAACCTT 240
QY 241 agttccgcctgtacgaccagtgcggtgttgatgcagaagtcacacagaccgaaac 300
Db 241 AGTTCCGCCTGTACGACCACTGCGGTGTTGATGTCAGAGTGCACACAGACCCGGAAC 300
QY 301 caggtaggaaaagttgggggagggcttcgtggtgggggtaaggagcagaggagagagac 360
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 Db 301 CAGGTAGGAAGTTGGGGAGGCTTCGTTGGGGGTAAAGGACAGAGAGAGAGAC 360
 QY 361 ccgggtgagcagcctccacaacaccgcaactctcttccaaagcacagggcagggatcc 420
 Db 361 CCGGGTGAGCAGCCTCCACAACACCACACTCTCTTTTCCAAAGCACAGGAGGATCC 420
 QY 421 tgcctcggcagacaggggtgagagaggttaagggtctggtgagtgagggcctaca 480
 Db 421 TGCCCTCGGCACAGCGGGTGGCGGAGAGGTAAAGGGGTCTGGGTGAGTGGGGCTACA 480
 QY 481 gcaagttagatgagcccttccctcctcctcctggtgtgtcctcaagagatctcttagtgt 540
 Db 481 CCACTCTAGATGAGGCCCTTCCCTCTCTCTCGGTGTGTCTCAAGAGATCTCTTAGTGT 540
 QY 541 cattcaccactgcaaaagagcccgaggttttactgcatcatcaatcaagttgctgaagggtcc 600
 Db 541 CATTTCAACCACCTGCAAGAGAGCCAGGTTTACTGCATCATCAAGTTGCTGAAGGGTCC 600
 QY 601 agccttaagtggcctctcttctcctcctcaggtcctcgggtcaacttaaggatagcc 660
 Db 601 AGCCTTAAGTGGCCCTCTTTCTGCCCTCAGGTCTCGCGGCTAAACTCTAAGGATAGGC 660
 QY 661 catcctcctgctgggtcagacacctggaggtcacctgaattggagccctctgtacctatc 720
 Db 661 CATCCTCTGCTGGGTGAGGCTGAGGCTCAGCTGACCTGAATGGAGCCCTCTGTACCTATC 720
 QY 721 tgggcaacaaagaaactaccatgaggtgggacaaatgagctcccaacacacagctt 780
 Db 721 TGGGCAACAAAGAAAGCTACCATGAGGCTGGGACAAATGAGCTCCCAACACACAGCTT 780
 QY 781 tggctcacatgaggtcacacttgatatacccccagtggtgaggtgaggttatgca 840
 Db 781 TGGTCCACATGATGGTGCACACTTGGATATACCCAGGTGGGTAAAGTTGGGGTATTGCA 840
 QY 841 gggcctcccaacatctctttaaataaaagaggtgtgtcaggttaaaaaa 900
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 QY 901 aaaaaa 938
 Db 901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 938

RESULT 2

V27158 ID V27158 standard; DNA; 1930 BP.
 AC V27158;
 DT 29-SEP-1998 (first entry)
 DE Unspliced murine NR6 nucleotide sequence.
 KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
 KW cell survival; therapeutic; neuronal proliferation; drug screening; ss;
 KW Mouse.
 OS MUS SP.
 PN W09811225-A2.
 PD 19-MAR-1998.
 PF 11-SEP-1997; G02479.
 PR 11-SEP-1996; AU-002246.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA (DZIE/) DZIELEWSKA H E.
 PI Alexander W, Fabry L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willison T,
 PI Zhang J;
 DR WPI; 98-260970/23.
 PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PT e.g. neuronal cells
 PS Example 8; Page 99-100; 182pp; English.
 CC NR6 is a novel haemopoietin receptor (HR). Interaction between the novel
 CC HR and a ligand facilitates proliferation, differentiation and survival
 CC of a wide variety of cells. The HR and its derivatives can be used for
 CC modulating the activity of the receptors e.g. to regulate development,
 CC maintenance or regeneration in an array of different cells and tissues in

CC vitro and in vivo. They can be present in therapeutics used for
 CC modulating neuronal proliferation, differentiation and survival. The
 CC products can also be used for detection and diagnosis, e.g. for cancers
 CC or predisposition to cancers, or for drug screening.
 SQ Sequence 1930 BP; 375 A; 623 C; 561 G; 371 T;

Query Match 94.7%; Score 888; DB 1: Length 1930;

Best Local Similarity 100.0%; Pred. No. 3.2e-160; Mismatches 0; Indels 0; Gaps 0;
 Matches 888; Conservative 0;

QY 1 ggcacgcttactctcgaagtgcttaaccattcgggatctatgggtcgaaaaag 60
 Db 1043 GGCACCGTTTACTTCGTCCAAGTGGTGTTRACCCATTTCGGGATCTATGGTTCGAAAAAG 1102
 QY 61 gcgggaatctggagagtgagccacccaccctgctccaccctcgaagtgaagcgc 120
 Db 1103 GCGGAATCTGGAGGAGTGGAGCCACCCACCGCTGCTCCACCCCTCGAAGTGAGCGC 1162
 QY 121 ccgggcccggcggggtgtgagccgaggggggggggggggggggggggggggg 180
 Db 1163 CCGGGCCCCGGGGGGGGGTGTGGAGCCGGGGGGGGGGGGGGGGGGGGGGGG 1222
 QY 181 cggcgagctcaagcagttctctcggtcggtcaagaagcagcgcatactgtctgaacctt 240
 Db 1223 CCGCGGAGCTCAAGCAGTCTCTCGGCTGGCTCAAGAAGCAGCAGCATCTGCTCGAACCTT 1282
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 QY 301 caggtaggaagttggggagggcttgcgtgggggggggggggggggggggggggg 360
 Db 1343 CAGGTAGGAAGTTGGGGGAGGCTTGCCTGGGGGGTAAAGGAGCAGAGAGAGAGAC 1402
 QY 361 ccgggtgagcagctcccaacacacccgctctcttccaaagcacagggcagggatcc 420
 Db 1403 CCGGGTGGAGCAGCTCCACACACCGCAGCTCTCTTTTCCAAAGCACAGGAGGATCC 1462
 QY 421 tgcctcggcgagcaggggtgcggcagaggttaagggtggtggtggtggtggtggt 480
 Db 1463 TGCCCTCGGCAGAGCGGGGTGGCGGAGAGGTAAAGGGGGTCTGGGTGAGTGGGGCTACA 1522
 QY 481 gcagctagatgagcccttctcctcctcctcctcctcctcctcctcctcctcct 540
 Db 1523 GCAGTCTAGATGAGGCCCTTTCCCTCTCTCTGCTTGTCTCAAGGGATCTCTTAGTGTCT 1582
 QY 541 cattcacccactgcaaaagagcccgaggttttactgcatcatcaagttgctgaagggtcc 600
 Db 1583 CATTTCAACCACCTGCAAGAGAGCCCGAGGTTTACTTGCATCATCAAGTTGCTCAAGGGTCC 1642
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 Db 1643 AGGCTTAATGTGGCCTCTTTCTTGCCTCAGGTCTCTCGCGCTAAACTCTAAGGATAGGC 1702
 QY 661 catcctcctgctgggtcagacacctgaggtcctcgaattgagccctctctaccctatc 720
 Db 1703 CATCTCTCTGCTGGGTTCAGACCTGGAGGCTCACCTGAAATGGAGCCCTCTCTGACTATC 1762
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 Db 1763 TGGGCNAACAAAGAACCTACCATGAGGCTGGGGCAGACATGAGCTCCCAACACACAGCTT 1822
 QY 781 tggctcacatgaggtcacacttgatatacccccaggtggtggtggtggtggtggt 840
 Db 1823 TGGTCCACATGATGGTGCACACTTGGATATACCCAGGTGGGTAAAGTTGGGGTATTGCA 1882
 QY 841 gggcctcccaacatctctttaaataaaagaggtgtgtcaggttaaaaa 888
 Db 1883 GGGCCTCCCAACATCTCTTTAAATAAATAAGAGGTGTGTTCAGGTAA 1930

RESULT 3

V27148
 ID V27148 standard; DNA; 11832 BP.
 AC V27148;
 DT 29-SEP-1998 (first entry)
 DE Nucleotide sequence for murine NR6 containing additional 5N sequence.
 KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
 KW cell survival; therapeutic; neuronal proliferation; drug screening; ss;
 KW Mouse.
 OS Mus sp.
 PN WO9811225-A2.
 PD 19-MAR-1998.
 PF 11-SEP-1997; G02479.
 PR 11-SEP-1996; AU-002246.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA (DZIE/) DZIEGLEWSKA H E.
 PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
 PI Zhang J.
 PI WPI: 98-260970/23.
 DR New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PT e.g. neuronal cells
 PS Claim 9; Fig 3; 182pp; English.
 CC The NR6 protein is a novel Haemopoietin receptor (HR). Interaction
 CC between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and it's
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 11832 BP; 2447 A; 3367 C; 3298 G; 2720 T;

Query Match 78.8%; Score 738.8; DB 1; Length 11832;
 Best Local Similarity 96.3%; Pred. No. 7.3e-132;
 Matches 778; Conservative 0; Mismatches 27; Indels 3; Gaps 2;

QY 79 tggagccacccaccctcctccaccctcctgaagtgagcgccggcgccggcgccggcg 138
 DB 10983 TGCCCGCGCCCAACACTGCGGCTCCATTCTTTTAAAGCGCCGCGCGCGCGCGG 11042
 QY 139 gtgtgcagcgcgggcgccgagccagctcgggccggtgcggcgagctcaagcag 198
 DB 11043 GTGTGCGAGCGCGCGCGGAGCCAGCTCGGGCCGCGTGGCGCGGAGCTCAAGCAG 11102
 QY 199 ttctcgggtggtcgaagcagcgcatactgtcgaaccttagtttccgcctgtacgac 258
 DB 11103 TTCTCGGCTGGCTCAAGAAGCAGCAGCTAGTCTGAACCTTAGTTTCGCCGTAGCAG 11162
 QY 259 caatggcggttgatgcagaagtcacacagacccgaaaccaggttagaaagtgggg 318
 DB 11163 CAGTGGCGTGTGGATGAGAGAGTCAACAAGACCCGAACCCAGTAGAAGATTGGGG 11222
 QY 319 gaggcttgctgggggttaagagcagagagagagacccgggtgaagcagctcca 378
 DB 11223 GAGGCTTGCTGGGGGTAAAGAGCAGAGAGAGAGACCCGGGTGAGCAGCCTCCA 11282
 QY 379 caacacccgcactcttttccaagcacagagagaggtatccttcgctcgggcagagcgg 438
 DB 11283 CAACACCGCAGCTCTTTTCCAAGCAGCAGCAGGAGGATCTTCCTCGGCGAGCGGG 11342
 QY 439 gtgcggcgagaggttaagggggttggtgagtgggcctacagcagcttagatgagcc 498
 DB 11343 GTGCGCGAGAGGTAAAGGGGGTGTGGGTGAGTGGGGCTACAGAGCTAGATGAGGCC 11402
 QY 499 ttctccctctcgtgtgtgtcgaagagctcttagtgcattatcccaactcaaa 558
 DB 11403 TTTCCTCTCTCGGGTGTGCTCAAAAGGATCTCTTAGTGCTCATTTACCCACTCAAA 11462
 QY 559 gagccccaggttttactgcatcatcaagtgtgtgaagggtccagggttaattggcctct 618

DB 11463 GAGCCCGAGGTTTTACTGTCATCATCAAGTTGCTGAAGGGTCCAGGCTTATATGTCCTCT 11522
 QY 619 ttctgcctcaggtcctgcggcctaaacttaagatagagcctcctcctcgtggtca 678
 DB 11523 TTTTGCCTCAGGTCCTCGGCTAACTCTAAGGATAGGCTCCTCTGCTGGGTCA 11582
 QY 679 gacctgaggtcctcactgaattgagccctctgtacctatctgggcaacaagaacct 738
 DB 11583 GACTGGAGGCTCACCCTGAATTGGAGCCCTCTGTACC-ATCTGGGCAACAAGAACCT 11641
 QY 739 accatgaggtcggggcacaatgagctccacacacacagcttttgggtccacataggtca 798
 DB 11642 ACCA--GAGGCTGGGCACATGAGCTCCACACACACAGCTTTGGTCCACATGATGTC 11699
 QY 799 cacttgatataccacagtggtggtgaaggttggtgattgcaggggctcccaaatctc 858
 DB 11700 CACTTGGATATACCCAGTGTGGGTAGGTGTTGGGTATTGCAGGGGCTCCCAAGAGTCTC 11759
 QY 859 tttaataataaaggaggtgttcaggt 886
 DB 11760 TTTAATAATAAAGGAGTGTTCAGGT 11787

RESULT 4
 V27145
 ID V27145 standard; DNA; 6663 BP.
 AC V27145;
 DT 02-OCT-1998 (first entry)
 DE Nucleotide sequence of Murine NR6.
 KW Haemopoietin receptor; cell proliferation; cell differentiation;
 KW cancer; cell survival; therapeutic; neuronal proliferation; drug;
 KW screening; ss; Mouse.
 OS Mus sp.
 FH Key
 FT CDS
 FT 1182..1744
 FT /*tag- a
 FT /product- "Murine NR6"
 FT /note- "No start or stop codon given"
 PN WO9811225-A2.
 PD 19-MAR-1998.
 PF 11-SEP-1997; G02479.
 PR 11-SEP-1996; AU-002246.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA (DZIE/) DZIEGLEWSKA H E.
 PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
 PI Zhang J.
 PI WPI: 98-260970/23.
 DR P-PSDB: W55016.
 PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PT e.g. neuronal cells
 PS Claim 8; Page 108-114; 182pp; English.
 CC The NR6 gene encodes a novel Haemopoietin receptor (HR). Interaction
 CC between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and it's
 CC products can be used for modulating the activity of the receptors e.g. to
 CC regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 6663 BP; 1462 A; 1852 C; 1715 G; 1634 T;

Query Match 78.8%; Score 738.8; DB 1; Length 6663;
 Best Local Similarity 96.3%; Pred. No. 6.8e-132;
 Matches 778; Conservative 0; Mismatches 27; Indels 3; Gaps 2;

QY 79 tggagccacccaccctcctccaccctcctgaagtgagcgccggcgccggcgccggcg 138
 DB 5814 TGCCCGCGCCCAACACTGCGGCTCCATTCTTTTAAAGCGCCGCGCGCGCGCGG 5873

DR WPI: 98-260970/23.
 DR P-PSDB; W55012.
 PT New isolated haematopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PT e.g. neuronal cells
 PS Claim 5: Page 84-87; 182pp; English.
 CC The haematopoietin receptor (HR) NR6.2 is a form of the novel HR NR6.
 CC Interaction between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and its
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 1673 BP; 344 A; 550 C; 474 G; 305 T;

Query Match 32.4%; Score 304; DB 1; Length 1673;
 Best Local Similarity 100.0%; Pred. No. 1.3e-49;
 Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ggcaaccttacttcgcaagtcgcttgaaccattcgggatctatgggtcgaaaaag 60
 DB 1043 GGCACCGTTTACTTCGTCCAGTGGCTTGTAACCCATTGCGGATCTATGGGTGCAAAAAG 1102
 QY 61 gcggaatctgagcagtgagtgagcaccacccacccgctgcctccaccctcgaaagtgcgc 120
 DB 1103 GCGGGAATCTGGAGCAGTGGAGCCACCCACCGCTGCCCTCCACCCCTCGAAGTAGCGC 1162
 QY 121 ccgggcccggcgggggtgtgtagcgcgcggcgggcgagccagctcgggcccggtg 180
 DB 1163 CCGGGCCCGGGCGGGGTGTGCGAGCGCGGGCGGAGCCAGCTCGGGCCCGGTG 1222
 QY 181 csgcgagctcaagcagttcctcgtggtcgaagaagcagcagcagcagcagcagcagc 240
 DB 1223 CGCGCGAGCTCAAGCAGTTCCTCGGCTGGCTCAAGAAGCAGCAGTCTGCTGAACCTT 1282
 QY 241 agttccgctgtacgaccagtggtggtggtggtggtggtggtggtggtggtggtggtg 300
 DB 1283 AGTTCCGCGCTGTACGACGAGTGGCGTGTGGATGCGATGCGAAGTCACAGACCCGAAAC 1342
 QY 301 csgg 304
 DB 1343 CAGG 1346

RESULT 7
 ID V41688 standard; cDNA; 1656 BP.
 AC V41688;
 DE Nucleotide sequence of the murine U4 gene.
 KW Murine; U4 protein; haematopoietin receptor superfamily;
 KW cell proliferation; immune response; antibody; cell differentiation;
 KW autoimmune disease; cancer; allergy; ds.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT CDS 122..1399
 FT /*tag= a
 FT /product= "U4 protein"
 PN WO9831811-A1.
 PD 23-JUL-1998.
 PF 15-JAN-1998; U00334.
 PR 16-JAN-1997; US-784863.
 PA (GENY) GENETICS INST INC.
 PI Collins M, Donaldson DD, Neben T, Whitters M;
 DR WPI: 98-414109/35.
 DR P-PSDB; W59804.
 PT New nucleic acid encoding U4 haematopoietin receptor superfamily
 PT chain - potentially useful, e.g. for modulating cell proliferation
 PT or immune response, for treating cancer and autoimmune disease
 PS Claim 1; Pages 25-26; 38pp; English.

CC This is the nucleotide sequence encoding the murine U4 protein from
 CC the haematopoietin receptor superfamily, used in the method of the
 CC invention for the modulation of cell proliferation, or the immune
 CC response. Transformed mammalian cells are used to produce recombinant
 CC U4 protein. The U4 protein is used to screen for specific binding
 CC agents, raise antibodies. It is also used as reagents for assays and
 CC as tissue markers for isolation of cognate ligands and receptors, and
 CC in pharmaceutical compositions which may modulate cell proliferation,
 CC cell differentiation, and the immune system (e.g. for treating immune
 CC deficiency, inherited or the result of infection, autoimmune diseases,
 CC cancer, and allergy).
 SQ Sequence 1656 BP; 318 A; 552 C; 478 G; 308 T;

Query Match 32.4%; Score 304; DB 1; Length 1656;
 Best Local Similarity 100.0%; Pred. No. 1.3e-49;
 Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ggcaaccttacttcgcaagtcgcttgaaccattcgggatctatgggtcgaaaaag 60
 DB 1040 GGCACCGTTTACTTCGTCCAGTGGCTTGTAACCCATTGCGGATCTATGGGTGCAAAAAG 1099
 QY 61 gcggaatctgagcagtgagtgagcaccacccacccgctgcctccaccctcgaaagtgcgc 120
 DB 1100 GCGGGAATCTGGAGCAGTGGAGCCACCCACCGCTGCCCTCCACCCCTCGAAGTAGCGC 1159
 QY 121 ccgggcccggcgggggtgtgtagcgcgcggcgggcgagccagctcgggcccggtg 180
 DB 1160 CCGGGCCCGGGCGGGGTGTGCGAGCGCGGGCGGAGCCAGCTCGGGCCCGGTG 1219
 QY 181 csgcgagctcaagcagttcctcgtggtcgaagaagcagcagcagcagcagcagcagc 240
 DB 1220 CGCGCGAGCTCAAGCAGTTCCTCGGCTGGCTCAAGAAGCAGCAGTCTGCTGAACCTT 1279
 QY 241 agttccgctgtacgaccagtggtggtggtggtggtggtggtggtggtggtggtggtg 300
 DB 1280 AGTTCCGCGCTGTACGACGAGTGGCGTGTGGATGCGAAGTCACAGACCCGAAAC 1339
 QY 301 csgg 304
 DB 1340 CAGG 1343

RESULT 8
 ID V70896 standard; cDNA; 1724 BP.
 AC V70896;
 DT 17-MAR-1999 (first entry)
 DE CDNA encoding rat Zcytor5.
 KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; zcytor5 ligand; ss.
 OS Rattus sp.
 FH Key Location/Qualifiers
 FT CDS 159..1436
 FT /*tag= a
 FT /product= zcytor5
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 DR P-PSDB; W70862.
 PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
 PT down-regulating Zcytor5 natural ligands or detecting cardiostrophin-1
 PT in blood
 PS Disclosure; Page 72-75; 55pp; English.

CC The present sequence encodes a protein designated Zcytor5, which is
 CC a cytokinin-like receptor. Soluble Zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytor5 could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible Zcytor5 ligands. A probe
 CC comprising Zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytor5 and
 CC therapeutically to modify Zcytor5 ligand effects.
 SQ Sequence 1724 BP; 350 A; 550 C; 500 G; 324 T;

Query Match 31.7%; Score 297.6; DB 1; Length 1724;
 Best Local Similarity 98.7%; Pred. No. 2.2e-48;
 Matches 300; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ggcacgtttacttcacagtcgctgttaacccttcggtggtcgaagaaag 60
 DB 1077 ggcacgtttacttcgctcgaagtcggtgttaacccttcggtggtcgaagaaag 1136
 QY 61 ggggaatctggagcagtcggtgagccacccacccgctgctccaccctcgaagtcgagcgc 120
 DB 1137 ggggaatctggagcagtcggtgagccacccacccgctgctccaccctcgaagtcgagcgc 1196
 QY 121 cggggccggggcggggggtgtcgcagccgcccggggcgagccagtcgagccggcggtg 180
 DB 1197 cggggccggggcggggggtgtcgcagccgcccggggcgagccagtcgagccggcggtg 1256
 QY 181 cggcgagcgtcaagcagtcctcgcgtgctcaagaagcagcagtcagtcgagccctt 240
 DB 1257 cggcgagcgtcaagcagtcctcgcgtgctcaagaagcagcagtcagtcgagccctt 1316
 QY 241 agttccgcctgtacgaccagtcggtgcttggatgcagaagtcacacagaccgaaac 300
 DB 1317 agttccgcctgtacgaccagtcggtgcttggatgcagaagtcacacagaccgaaac 1376
 QY 301 cagg 304
 DB 1377 cagg 1380

RESULT 9
 ID V27144 standard; cDNA; 1391 BP.
 AC V27144;
 DT 29-SEP-1998 (first entry)
 DE Nucleotide sequence of clone HFK-66 encoding human NR6.
 KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
 KW cell survival; therapeutic; neuronal proliferation; drug screening; ss;
 KW Human.
 OS Homo sapiens.
 FH Key
 FT CDS
 FT 1..1053
 FT /tag- a
 FT /product- "Human NR6"
 FT
 PN W09811225-A2.
 PD 19-MAR-1998.
 PF 11-SEP-1997; G02479.
 PR 11-SEP-1996; AU-002246.
 PR (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA (DZIE/) DZIELEWSKA H E.
 PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
 PI Zhang J;
 DR WPI: 98-260970/23.
 DR P-PSDB: W55015.
 DR PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PT e.g. neuronal cells
 PS Claim 7; Page 102-104; 182pp; English.
 CC The NR6 gene encodes a novel Haemopoietin receptor (HR). Interaction

CC between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and its
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 1391 BP; 281 A; 459 C; 417 G; 234 T;

Query Match 26.6%; Score 249.8; DB 1; Length 1391;
 Best Local Similarity 86.8%; Pred. No. 2.4e-39;
 Matches 275; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 ggcacgtttacttcgctcgaagtcggtgtaacccttcggtggtcgaagaaag 60
 DB 682 ggcacgtttacttcgctcgaagtcggtgtaacccttcggtggtcgaagaaag 741
 QY 61 ggggaatctggagcagtcggtgagccacccacccgctgctccaccctcgaagtcgagcgc 120
 DB 742 ggggaatctggagcagtcggtgagccacccacccgctgctccaccctcgaagtcgagcgc 801
 QY 121 cggggccggggcggggggtgtcgcagccgcccggggcgagccagtcgagccggcggtg 180
 DB 802 cggggccggggcggggggtgtcgcagccgcccggggcgagccagtcgagccggcggtg 861
 QY 181 cggcgagcgtcaagcagtcctcgcgtgctcaagaagcagcagtcagtcgagccctt 240
 DB 862 cggcgagcgtcaagcagtcctcgcgtgctcaagaagcagcagtcagtcgagccctt 921
 QY 241 agttccgcctgtacgaccagtcggtgcttggatgcagaagtcacacagaccgaaac 300
 DB 922 agttccgcctgtacgaccagtcggtgcttggatgcagaagtcacacagaccgaaac 981
 QY 301 caggtaggaaagtggg 317
 DB 982 caggtaggaaagtggg 998

RESULT 10
 ID V70895 standard; cDNA; 1813 BP.
 AC V70895;
 DT 17-MAR-1999 (first entry)
 DE cDNA encoding an allelic variant of human Zcytor5.
 KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 KW cardiac pathology; heart enlargement; Zcytor5 ligand; allelic variant;
 KW ss.
 OS Homo sapiens.
 FH Key
 FT CDS
 FT 88..1365
 FT /tag- a
 FT /product- zcytor5
 FT
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 DR P-PSDB: W70861.
 DR PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
 PT down-regulating Zcytor5 natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Disclosure: Page 68-70; 55pp; English.
 CC The present sequence encodes an allelic variant of protein designated
 CC Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be

CC blood, and to discover other possible zcytor5 ligands. A probe
CC comprising zcytor5 DNA or RNA can be used to determine the presence
CC and integrity of the zcytor5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify zcytor5 and
CC therapeutically to modify zcytor5 ligand effects.
SQ Sequence 1690 BP; 319 A; 592 C; 505 G; 274 T;

Query Match 26.6%; Score 249.6; DB 1; Length 1690;
Best Local Similarity 88.8%; Pred. No. 2.7e-39;
Matches 270; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1 ggcaccgttactctccaagtcgttgaaccattcggtggtatctatgggtcgaaag 60
DB 961 GGCACCGTGTACTCTGCAAGTGCCTGCAACCCCTTTGGCATCTATGCTCCAAAGAA 1020
QY 61 ggggaattctggagtgagtcacccacccagcgtccctccaccctcgaagtgcgc 120
DB 1021 GCCGGGATCTGGAGTGAAGTGGAGCCACCCACAGCCGCTCCACTCCCGCAGTGAGCGC 1080
QY 121 ccggggccggggcggggtgtgagcgccggggggggcgagcccgagctcgggcccggtg 180
DB 1081 CCGGGCCCGGGCGGGCGCTCGGAACCGCGGGCGGAGCGCGAGCTCGGGCCGGTG 1140
QY 181 cggcgagctcaagcagttctctcggtctcaagaagcagcgcatactgctgaacctt 240
DB 1141 CGGGCGAGCTCAAGCAGTTCCTGGGCTGGCTCAAGAAGCACGCTACTGCTCAACCTC 1200
QY 241 agttccgctgtacgaccagtggtgctgtgagtcaggaagtcacaaagaccgcaaac 300
DB 1201 AGTTCCGCTCTACGACCACTGGGAGCGCTGGATCGAGAAGTCGGCACAGACCCGCAAC 1260
QY 301 cagg 304
DB 1261 CAGG 1264

RESULT 13

V70897
ID V70897 standard; cDNA; 259 BP.
AC V70897; (first entry)
DT 17-MAR-1999 (first entry)
DE Expressed sequence tag used to identify human zcytor5.
KW zcytor5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
KW cardiac pathology; heart enlargement; zcytor5 ligand; EST; ss.
OS Unidentified.
PN WO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
DR WPI; 99-034662/03.
PT New mammalian cytokinin-like receptor zcytor5 - useful for, e.g.
PT down-regulating zcytor5 natural ligands or detecting cardiotoxin-1
PT in blood
PS Example 1; Page 77; 55pp; English.
CC The present sequence represents an expressed sequence tag (EST)
CC used to identify cDNA encoding a protein designated zcytor5, which is
CC a cytokinin-like receptor. Soluble zcytor5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
CC enlargement. zcytor5 could be used to detect cardiotoxin-1 in the
CC blood, and to discover other possible zcytor5 ligands. A probe
CC comprising zcytor5 DNA or RNA can be used to determine the presence
CC and integrity of the zcytor5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify zcytor5 and

CC therapeutically to modify zcytor5 ligand effects.
SQ Sequence 259 BP; 53 A; 64 C; 81 G; 46 T;
Query Match 9.9%; Score 92.8; DB 1; Length 259;
Best Local Similarity 76.8%; Pred. No. 1.1e-09;
Matches 106; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 1 ggcaccgttactctccaagtcgttgaaccattcggtggtatctatgggtcgaaag 60
DB 119 GGCACCGTGTACTCTGTCGAAGTGCCTGCAACCCCTTTGGCATCTATGCTCCAAAGAA 178
QY 61 ggggaattctggagtgagtcacccacccagcgtccctccaccctcgaagtgcgc 120
DB 179 GCCGGGATCTGGAGTGAAGTGGAGCCACCCACAGCCGCTTCANTTCCCGCAGTGAGCGN 238
QY 121 ccggggccggggcgggcgggg 138
DB 239 CNGGGCCCGGGGNGGG 256

RESULT 14

V09036
ID V09036 standard; RNA; 12827 BP.
AC V09036;
DT 21-JUL-1998 (first entry)
DE Equine arteritis virus partial RNA genome sequence.
KW equine arteritis; genome; EAV; detection; therapy; ss.
OS Equine arteritis virus.
PN WO9802549-A1.
PD 22-JAN-1998.
PF 14-JUL-1997; NL0408.
PR 12-JUL-1996; NL-003579.
PA (UYLE-) RIJKSUNIV LEIDEN.
PI Bredenbeek PJ, Den Boon JA, Snijder EJ, Spaan WJM,
PI Van Dinten LC, Wassenaar ALM;
DR WPI; 98-110596/10.
PT Recombinant DNA vector that produces infectious RNA of equine
PT arteritis virus - and derived RNA, host cells and virus particles,
PT useful therapeutically
PS Claim 1; pages 15-19; 36pp; English.
CC The sequence is that of at least part of the RNA genome of the equine
CC arteritis virus. It can be used in the construction of a recombinant
CC DNA vector comprising a DNA sequence complementary to part of
CC the genome of equine arteritis virus (EAV) which has
CC adjacent to its 3'-end a non-EAV specific promoter for a non-EAV
CC specific RNA polymerase. The RNA and the vector can be used to
CC make viral particles and for therapeutic use. The vector can be
CC stably incorporated into host cells and produces infectious RNA.
SQ Sequence 12827 BP; 2831 A; 3258 C; 3295 G; 3443 T;

Query Match 7.6%; Score 71.2; DB 1; Length 12827;
Best Local Similarity 71.1%; Pred. No. 2.2e-05;
Matches 108; Conservative 0; Mismatches 43; Indels 1; Gaps 1;
QY 788 catgatgtcacacttgatatacccccagtcgtg-gtaaggttggtggtatcgagggcct 846
DB 13618 CAGGCGGTGAAGCGTGGATATCTCTCTGTGCGCTCATGTTGAAGTAGTATTAGCCA 12677
QY 847 cccacaactctcttaataataaaggaggtgttccagggtataaataaataaataaataa 906
DB 12678 CCAGGACCAA 12737
QY 907 aaaaaaataaataaataaataaataaataaataaataaataaataaataaataaataa 938
DB 12738 AA 12769
RESULT 15
V09039
ID V09039 standard; DNA; 15528 BP.
AC V09039;

DT 21-JUL-1998 (first entry)
 DE Equine arteritis virus expression vector pEAV030.
 KW Equine arteritis; genome; EAV; detection; therapy; cyclic; circular;
 OS ds.
 OS Equine arteritis virus.
 OS Bacteriophage T7.
 OS Synthetic.
 FH Key
 FT Location/Qualifiers
 FT 15512..15528
 FT /*tag= a
 FT /note= "Bacteriophage T7 promoter sequence"
 FT misc_feature 12845..12851
 FT /*tag= b
 FT /note= "synthetic sequence with unique XhoI site"
 FT misc_feature 12852..15490
 FT /*tag= c
 FT /note= "pUC18 vector sequence"
 FT WO9802549-A1.
 PN 22-JAN-1998.
 PD 14-JUL-1997; NL0408.
 PF 12-JUL-1996; NL-003579.
 PR (UYLE-) RIJKSUNIV LEIDEN.
 PI Bredenbeek PJ, Den Boon JA, Snijder EJ, Spaan WJM,
 PI Van Dinten LC, Wassenaar ALM;
 DR WPI: 98-110596/10.
 PT Recombinant DNA vector that produces infectious RNA of equine
 PT arteritis virus - and derived RNA, host cells and virus particles,
 PT useful therapeutically
 PS Claim 4; Pages 21-24; 36pp; English.
 CC The sequence is that of a recombinant DNA vector, pEAV030,
 CC comprising a DNA sequence complementary to part of
 CC the genome of equine arteritis virus (EAV) which has
 CC adjacent to its 3'-end a non-EAV specific promoter for a non-EAV
 CC specific RNA polymerase. It can be used to make viral particles
 CC and for therapeutic use. The vector can be stably incorporated
 CC into host cells and produces infectious RNA.
 CC Sequence 15528 BP; 3492 A; 3941 C; 3972 G; 4123 T;
 SQ

Query Match 7.6%; Score 71.2; DB 1; Length 15528;
 Best Local Similarity 71.1%; Pred. No. 2.2e-05;
 Matches 108; Conservative 0; Mismatches 43; Indels 1; Gaps 1;
 Oy 788 catgatgttcacacttgatataccccagtggtg-gtaaggttggtggtattgcagggcct 846
 Db 12635 CAGGGCCGTAGACGCTGGATATTCCTGTGGCTCATGTGAAGTAGTTATTAGCCA 12694
 Oy 847 cccaacaatctcttaataataaaggaggtgttcaggtaaaaaaaaaaaaaaaaaaa 906
 Db 12695 CCCAGAACCCAAAAAaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 12754
 Oy 907 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 938
 Db 12755 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 12786

Search completed: September 28, 1999, 16:45:44
 Job time: 7329 sec

No.	Score	Match	Length	DB	ID	Description
1	64	6.8	10660	4	US-08-267-803B-8	Sequence 8, Appl
2	63.4	6.8	3581	4	US-08-738-349-1	Sequence 1, Appl
3	63.2	6.7	5173	2	US-08-242-677-1	Sequence 1, Appl
4	62.6	6.7	2628	2	US-08-143-219-1	Sequence 1, Appl
5	61.6	6.6	270	4	US-08-520-678A-30	Sequence 30, Appl
6	61.4	6.5	1558	3	US-08-467-607-2	Sequence 2, Appl
7	61.4	6.5	1558	4	US-08-469-362-2	Sequence 2, Appl
8	61.4	6.5	1558	4	US-08-850-392-2	Sequence 2, Appl
9	61	6.5	3238	5	PCT-US94-10080-5	Sequence 5, Appl
10	60.8	6.5	6671	2	US-08-280-443-1	Sequence 1, Appl
11	60.8	6.5	6671	2	US-08-457-459-1	Sequence 1, Appl
12	60.8	6.5	6671	3	US-08-555-678-1	Sequence 1, Appl
13	60.8	6.5	6671	5	PCT-US95-02275-1	Sequence 1, Appl
14	60.6	6.5	1817	1	US-08-473-981A-5	Sequence 1, Appl
15	60.6	6.5	2285	4	US-08-967-101-136	Sequence 5, Appl
16	60.6	6.5	903	5	PCT-US95-06406A-21	Sequence 136, App
17	60.4	6.4	1066	3	US-08-157-101A-4	Sequence 21, Appl
18	60.2	6.4	1046	1	US-08-361-467B-4	Sequence 4, Appl
19	60.2	6.4	1046	3	US-08-484-332C-4	Sequence 4, Appl
20	60.2	6.4	1166	5	PCT-US96-12129B-1	Sequence 1, Appl
21	60	6.4	1325	3	US-08-306-691B-51	Sequence 51, Appl
22	60	6.4	1325	4	US-08-464-517-1	Sequence 1, Appl
23	60	6.4	1325	5	PCT-US93-05000-1	Sequence 1, Appl
24	59.6	6.4	3214	1	US-08-484-105-17	Sequence 17, Appl
25	59.6	6.4	3214	1	US-08-484-106-17	Sequence 17, Appl
26	59.6	6.4	1738	4	US-08-379-482A-2	Sequence 2, Appl
27	59.2	6.3	2158	1	US-07-602-608-1	Sequence 1, Appl
28	59.2	6.3	2158	1	US-08-261-578-1	Sequence 1, Appl
29	59.2	6.3	2082	4	US-08-785-310A-2	Sequence 2, Appl
30	59.2	6.3	1461	5	PCT-US95-04258-4	Sequence 4, Appl
31	58.6	6.2	1172	1	US-07-945-288-9	Sequence 9, Appl
32	58.6	6.2	1172	1	US-08-462-831-9	Sequence 9, Appl
33	58.6	6.2	1641	1	US-08-300-903A-8	Sequence 8, Appl
34	58.6	6.2	140	1	US-08-628-417-5	Sequence 5, Appl
35	58.6	6.2	240	1	US-08-628-417-6	Sequence 6, Appl
36	58.6	6.2	144	2	US-08-702-344-26	Sequence 26, Appl
37	58.6	6.2	1172	3	US-08-461-809-9	Sequence 9, Appl

Db 10558 TATTGTTTCAGTATACCTCGTA

10558 TATTGTTTCAGTATACTCGTACTAATAAATAACACTGCCA

Db 3529 AAAAAAAAAAAAAAAAAAAAAA 3557

RESULT 3

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1 05-08-242-677-1
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1  CLASIFICATION: 435
2  ATTORNEY/AGENT INFORMATION:
3  NAME: Mayfield, Denise L.
4  REGISTRATION NUMBER: 33,732
5  REFERENCE/DOCKET NUMBER: UTSD:401
6  TELECOMMUNICATION INFORMATION:
7  TELEPHONE: 713-787-1400
8  TELEFAX: 713-789-2679
9  INFORMATION FOR SEQ ID NO: 1:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 5173 base pairs
12 TYPE: nucleic acid
13 STRANDEDNESS: single
14 TOPOLOGY: linear
15 MOLECULE TYPE: cDNA
16 FEATURE:
17 NAME/KEY: CDS
18 LOCATION: 1..4863
19 US-08-242-677-1

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Query Match      6.7%; Score 63.2; DB 2; Length 5173;
Best Local Similarity 84.5%; Pred. No. 1.1e-05;
Matches 71; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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RESULT 4
US-08-143-219-1
; Sequence 1, Application US/08143219
; Patent No. 5670330
; GENERAL INFORMATION:
; APPLICANT: Sonenberg, Nahum
; APPLICANT: Katze, Michael G.
; APPLICANT: Roy, Sophie
; APPLICANT: Koromilas, Antonis E.
;

RESULT 5
US-08-520-678A-30/c
; Sequence 30, Application US/08520678A
; Patent NO. 5874565
; GENERAL INFORMATION:
; APPLICANT: Rice, Charles M.
; APPLICANT: Kolykhalov, Alexander A.
; TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
; TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 39

SOFTWARE: PatentIn Release #1.0, version #1.30

RESULT 8
US-08-850-392-2
Sequence 2, Application US/08850392
Patent No. 585982
GENERAL INFORMATION:
APPLICANT: TUNG, JAY S.
APPLICANT: SINHA, SUKANTO
APPLICANT: MCCONLOGUE, LISA
APPLICANT: SEMKO, CHRISTOPHER M.F.
TITLE OF INVENTION: NOVEL CATHESPIN AND METHODS AND
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATHENA NEUROSCIENCES
STREET: 800 F. Gateway Blvd.
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850.392
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469.362
FILING DATE: 08-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: DUVALL, JEAN M.
REGISTRATION NUMBER: 32,731
REFERENCE/DOCKET NUMBER: 002010-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
TELEFAX: (415) 877-8370
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1558 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 103..1011
 US-08-850-392-2

Query Match 6.5%; Score 61.4; DB 4; Length 1558;
 Best Local Similarity 55.3%; Pred. No. 1.8e-05;

Matches 86; Conservative 13; Mismatches 56; Indels 0; Gaps 0;

QY 784 tccacatggtgcacactggatatacccccagtggtgtaagttgggtattgcagg 843

Db 1373 TCMCCATCTTATTTCACYTATAGATCMAGGGTGGGRGRGGGAGGAATTGTCTART 1432

QY 844 cctcccaacaatctttaaataataaagaggtgttcaggtataaaataaa 903

Db 1433 TCCCCMTCCCCCANTGNTGRAAAARAATCTGCCCTYCCCGAAAAA 1492

QY 904 aaaaaaataaaataaaataaaataaaataaaataaaataaa 938

Db 1493 AAAAAAAAAAAGAAAAAATAAA 1527

RESULT 9

PCT-US94-10080-5

; Sequence 5, Application PC/TUS9410080

; GENERAL INFORMATION:

; APPLICANT: GENETICS INSTITUTE, INC.

; TITLE OF INVENTION: RECEPTOR PROTEINS

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute Inc. - Legal Affairs

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: USA

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/10080

; FILING DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/123,934

; FILING DATE: 17-SEP-1993

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: LAZAR, Steven R

; REGISTRATION NUMBER: 32,618

; REFERENCE/DOCKET NUMBER: 5203-PCT

; TELEPHONE: (617) 498-8260

; TELEFAX: (617) 876-5851

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3238 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; IMMEDIATE SOURCE:

; CLONE: CFK1-10a

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 474..2000

; PCT-US94-10080-5

Query Match 6.5%; Score 61; DB 5; Length 3238;

Best Local Similarity 82.4%; Pred. No. 2.8e-05;

Matches 70; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 854 atctcttaataataaagaggtgttcaggtataaaataaaataaaataaa 913

Db 3127 ATTGTGTAATAATAATAACTGTTTCAAGTCAAAAAAAAAAAAAAAAAA 3186

QY 914 aaaaaaataaaataaaataaaataaaataaaataaa 938

Db 3187 AAAAAAAAAAAAAAAAAAATA 3211

RESULT 10

US-08-280-443-1

; Sequence 1, Application US/08280443

; Patent No. 5643778

; GENERAL INFORMATION:

; APPLICANT: Nishikura, Kazuko

; TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use

; TITLE OF INVENTION: Thereof

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Howson and Howson

; STREET: Spring House Corporate Cntr, P.O. Box 457

; CITY: Spring House

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19477

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/280,443

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/197,794

; FILING DATE: 17-FEB-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Bak, Mary E

; REGISTRATION NUMBER: 31,215

; REFERENCE/DOCKET NUMBER: WST49AUSA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-540-9206

; TELEFAX: 215-540-5818

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6671 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: unknown

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 155..3832

; US-08-280-443-1

Query Match 6.5%; Score 60.8; DB 2; Length 6671;

Best Local Similarity 80.7%; Pred. No. 3.9e-05;

Matches 71; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 851 acaatctttaaataaataaagaggtgttcaggtataaaataaaataaaataaa 910

Db 6538 ACATTCTCTATAATAAAAAAAAAAARCAAGAATCTGAATAAAAAAAAAA 6597

QY 911 aaaaaaataaaataaaataaaataaaataaaataaa 938

Db 6598 AAAAAAAAAAAAAAAAAAATA 6625

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RESULT 12
US-08-555-678-1
; Sequence 1, Application US/08555678
; Patent No. 5763174
; GENERAL INFORMATION:
; APPLICANT: Nishikura, Kazuko
; TITLE OF INVENTION: RNA Editing Enzyme and Methods

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[illegible]

RESULT 15
US-08-967-101-136
Sequence 136, Application US/08967101
Patent No. 5840540
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESSES:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 28, 1999, 15:38:09 ; Search time 2095.87 seconds
(without alignments)
882.801 Million cell updates/sec

Title: US-09-037-657-16

Perfect score: 938

Sequence: 1 ggcaccgttactctgtcca.....aaaaaaaaaaaaaaaaaaaa 938

Scoring table: IDENTITY_NUC

Searched: 2846578 seqs, 986266752 residues

Database :

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2: em_est2:*

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7: em_est7:*

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22: gb_est3:*

23: gb_est4:*

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26: gb_est7:*

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57: em_est25:*

58: em_est26:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	236.6	25.2	503	29	AA049278	AA049278 m145c04.r
C 2	231.8	24.7	445	27	AA039053	AA039053 m199d07.r
C 3	194.2	20.7	262	50	AV032198	AV032198 AV032198
C 4	187.6	20.0	458	27	AA043001	AA043001 A256f01.r
C 5	185.4	19.8	390	26	W17583	W17583 mb75b01.r1
C 6	168	17.9	455	46	AA925924	AA925924 UI-R-Al-e
C 7	151	16.1	470	43	AI233311	AI233311 EST229999
C 8	150	16.0	229	49	AV010798	AV010798 AV010798
C 9	137.4	14.6	464	41	AI071408	AI071408 UI-R-C2-n
C 10	135.8	14.5	167	49	AV011309	AV011309 AV011309
C 11	108.2	11.5	247	32	AA377893	AA377893 EST90550
C 12	101	10.8	234	47	AI535068	AI535068 UI-R-C3-s
C 13	100.2	10.7	404	42	AI074921	AI074921 oy04d08.s
C 14	92.4	9.9	482	26	W66776	W66776 mel17b11.r1
C 15	85	9.1	227	30	AA270365	AA270365 va63b12.r
C 16	69.8	7.4	376	46	AI433590	AI433590 t147a10.x
C 17	68.8	7.3	196	45	AI352274	AI352274 q12c06.x
C 18	68.2	7.3	325	48	AI589091	AI589091 tf80h04.x
C 19	68.2	7.3	319	50	AI682968	AI682968 tw47q04.x
C 20	68	7.2	358	44	AI271796	AI271796 q182b10.x
C 21	67.8	7.2	394	45	AI371009	AI371009 ta07b11.x
C 22	67.8	7.2	358	47	AI539766	AI539766 cp77e03.x
C 23	67.4	7.2	263	44	AI244343	AI244343 q176a04.x
C 24	66.4	7.1	250	46	AI417790	AI417790 th31d09.x
C 25	66.4	7.1	305	47	AI521040	AI521040 to70b06.x
C 26	66.4	7.1	231	47	AI523973	AI523973 t998h03.x
C 27	66.4	7.1	458	47	AI537863	AI537863 tp32e01.x
C 28	66.4	7.1	371	48	AI587156	AI587156 ts5a04.x
C 29	66.4	7.1	311	49	AI621179	AI621179 tu88e05.x
C 30	66.2	7.1	153	34	AA464646	AA464646 zx85b11.r
C 31	66.2	7.1	254	37	AA697665	AA697665 HL02953.f
C 32	66.2	7.1	401	51	AI722398	AI722398 fc26e05.x
C 33	66	7.0	190	30	AA270119	AA270119 va60h03.r
C 34	66	7.0	368	37	AA674904	AA674904 vq57c09.r
C 35	66	7.0	572	44	AI255307	AI255307 ui19d03.x
C 36	65.8	7.0	290	28	AA083230	AA083230 zn31h04.s
C 37	65.8	7.0	225	45	AI358213	AI358213 qv96h06.x
C 38	65.8	7.0	264	49	AI626954	AI626954 vs79h10.x
C 39	65.8	7.0	669	53	HS0005112	AL040636 Homo sapi
C 40	65.6	7.0	150	35	AA590718	AA590718 vn59g09.r
C 41	65.6	7.0	236	44	AI286236	AI286236 qu91a07.x
C 42	65.6	7.0	273	44	AI290128	AI290128 qw31e07.x
C 43	65.6	7.0	646	49	AI635457	AI635457 ts65b04.x
C 44	65.6	7.0	518	50	AI696969	AI696969 wc76d02.x
C 45	65.4	7.0	215	46	AI445611	AI445611 tj08a03.x

ALIGNMENTS

RESULT 1
AA049278/c
LOCUS AA049278 503 bp mRNA
DEFINITION m145c04.r1 Soares mouse embryo NmME13.5 14.5 Mus musculus cDNA
clone IMAGE:479046 5', mRNA sequence.
ACCESSION AA049278
NID g1755309
VERSION AA049278.1 GI:1755309

30-DEC-1996

Db 265 AGGTCCTGCCGGCTAAACTTAAGATAGGCGCATCCCTCCTCTGGGTGAGACCTGGAGGC 206
 QY 690 tcacctgaattggagccctctgtacacctatctgggcaacaagaatacctacatgagcct 749
 Db 205 TCACCTGAATTGGAGCCCTCTGTACC-ATCTGGGCAACAAGAAACCTACCA-GAGGCT 148
 QY 750 ggggcaaatgagctccacacacacacagcttgggtccacatgatggtccacacttggatat 809
 Db 147 GGGGCAAAATGAGCTCCCAACACACAGCTTTGGTCCACATGATGTCACACTTGGATAT 88
 QY 810 acccagctgggtaaggttgggtattgagggcctcccaacaatctcttaataaat 869
 Db 87 ACCCAGTGTGGTGGGTGGGTATGAGGGCCCTCCCAAGAGTCTCTTTAATAAAT 28
 QY 870 aaaggagtttcaggttaaaaaa 896
 Db 27 AAAGGAGTTGTCAGGTCCCGAAAAA 1

RESULT 3

AV032198 262 bp mRNA EST 03-JUN-1999
 LOCUS AV032198 Mus musculus adult C57BL/6J cerebellum Mus musculus CDNA
 clone 1500034F20, mRNA sequence.
 ACCESSION AV032198
 NID 94831746
 VERSION AV032198.1 GI:4831746
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 262)
 AUTHORS Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Ito,M., Aizawa,K.,
 Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T.,
 Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,T.,
 Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H.,
 Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y.,
 Sugahara,Y., Suzuki,H., Suzuki,H., Tateo,M., Tomaru,Y.,
 Tomimaga,N., Watanabe,S., Yagane,M., Yamamura,T., Yokota,T.,
 Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
 RIKEN Mouse ESTs
 Unpublished (1999)
 COMMENT On Jun 22, 1998 this sequence version replaced gi:3246782.

Contact: Chile Owa
 Genome Science Laboratory
 RIKEN
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098
 Email: genome-res@rtc.riken.go.jp
 Thermostabilization and thermostimulation of thermolabile enzymes by
 trehalose and its application for the synthesis of full length cDNA
 (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for
 further details.

FEATURES

Location/Qualifiers
 1..262
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="1500034F20"
 /clone_lib="Mus musculus adult C57BL/6J cerebellum"
 /sex="male"
 /tissue_type="cerebellum"
 /dev_stage="adult"
 63 a 63 c 69 g 67 t

BASE COUNT
 ORIGIN

Query Match 20.7% Score 194.2; DB 50; Length 262;
 Best Local Similarity 91.9%; Pred. No. 1.7e-27;
 Matches 238; Conservative 0; Mismatches 18; Indels 3; Gaps 3;
 QY 629 caggtcctgcggctaaactctaaagtaggagccatctcct-gctgggtcagacctggag 687
 Db 2 CACGTTCTGGGGGTTAACTATTAGGATCGGCTATCCTCTCGCTGGGTTAGACCTGGAG 61
 QY 688 gctcacctgaatggagccctctgtacctatctgtgggcaacaagaacctaccatgagg 747
 Db 62 GTCACCTGAATGGAGCCCTTTGTACC-ATTTGGCAACAAGAAACCTACCA-GAGG 119
 QY 748 ctggggcaccaatgagctcccaacacacacagctttggccacatgatggtcacacttggat 807
 Db 120 CTGGGCGACATGAGCTCCCAACACACAGCTTTGGTCCACATGATGGTCACACTTGGAT 179
 QY 808 ataccacagtggtgtaaggttgggtattgagggcctcccaacaatctcttaataa 867
 Db 180 ATACCCAGTGTGGGTAGGTTGGGTATTGCGAGGGCTCCCAAGAGTTTCTTTAATAA 239
 QY 868 ataaaggagttgttcaggt 886
 Db 240 ATAAAGGAGTTGTTCAGGT 258

RESULT 4

AA043001/C
 LOCUS AA043001 458 bp mRNA EST 10-MAY-1997
 DEFINITION zk56f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens CDNA clone
 IMAGE:486841 5', mRNA sequence.
 ACCESSION AA043001
 NID 91522545
 VERSION AA043001.1 GI:1522545
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 458)
 AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
 Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
 Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le.N.,
 Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
 Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
 Trevisan,E., Underwood,K., Woldmann,P., Waterston,R., Wilson,R.
 and Marra,M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 97044478
 COMMENT On May 9, 1995 this sequence version replaced gi:802616.

Contact: Wilson RK

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: es@wustl.edu

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (infoimage.llnl.gov) for further information.

Insert Length: 1219 Std Error: 0.00

Seq primer: 28M13 rev2 from Amersham

High quality sequence stop: 305.

Location/Qualifiers

1..458
 /organism="Homo sapiens"
 /db_xref="GDB:376055"
 /db_xref="taxon:9606"
 /clone="IMAGE:486841"
 /clone_lib="Soares_pregnant_uterus_NbHPU"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: uterus; Vector: pT73-Pac; Site_1: Not I;

oligo-dt track served to identify it as a clone from the normalized adult brain library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics. The following repetitive elements were found in this cDNA sequence: 1-35, SPOLY_Asimple_repeat

FEATURES

Location/Qualifiers
1. .455
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-AI-es-g-11-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AI library is a subtracted library derived from the UI-R-A0 library. The UI-R-A0 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dt track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-AI) was constructed as follows: PCR amplified cDNA inserts from a pool of approximately 3,840 UI-R-A0 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-A0 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-AI library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)."

BASE COUNT 110 a 109 c 112 g 124 t
ORIGIN

Query Match 17.9%; Score 168; DB 46; Length 455;
Best Local Similarity 74.1%; Pred. No. 1.5e-22;
Matches 274; Conservative 0; Mismatches 75; Indels 21; Gaps 4;

QY 560 accccaggttttactgcatcatcaagtgtgtaagg-----tcagg 603
DB 369 AGCGTCAGGCTTCACTGCATCTCCAGTCTGCTGAAAGGAGTCTATCTCAAGACTCCAGG 310

QY 604 cttaatgtggctcttttgcctcaggtcctgcgggttaacttaaggtatggccat 663
DB 309 CTATATGTGGCTCTTTTCTGCCCTCAGGTCTCTGCGGTAACTTGAGGTAGGCCAT 250

QY 664 ctctctgtgggt-cagacctggaggctcacctgaattgtgagccctctgtac---ctat 719
DB 249 CCTCCTGCTGGATGAGACCTGGAGGCTCACCTGACTGGAGACCATCTGTACTGTCAT 190

QY 720 ctgggcaacaagaacctcacatgaggtg9gggcaaatgagctcccaaccacagct 779
DB 189 TTGGGCAATGAGAAACAACACAGGGGCTGGGGCAACATGAGTCCCAACACACAGCT 130

QY 780 ttggtccacatggttcacacttgatatacccaagtggtggttaagggtggtattgc 839
DB 129 TTGG-CCACATGATGCTAACCTTTTGATGTACCCCAATATGGGTAGGTTGGAGTAATGA 71

QY 840 agggctcccaacaactctcttaataaataaaggaggtgttgcaggtataaaaaa 899
DB 70 CRAAGGTTATGAGGACCCCTCCCAAGAGTCTCTTTGATAAATAAGAAAGAGTAAAAA 11

QY 900 aaaaaa 909
DB 10 AAAAAAAAAA 1

RESULT 7

AI233311/c
LOCUS AI233311.1
DEFINITION Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
ACCESSION AI233311
NID 3817191
VERSION AI233311.1 GI:3817191
KEYWORDS EST
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 470)
AUTHORS Lee N.H., Glodek A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT On May 8, 1995 this sequence version replaced gi:801255.

Contact: Lee, NH

ATCC

The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org

Seq primer: M13-21

FEATURES
source
1. .470
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RKIDD49"
/clone.lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT73Pac; Site_1: EcoRI;
Site_2: NotI"

BASE COUNT 88 a 143 c 124 g 115 t
ORIGIN

Query Match 16.1%; Score 151; DB 43; Length 470;
Best Local Similarity 96.9%; Pred. No. 2.3e-19;
Matches 154; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 146 agcccgggggcgagccagctcgcccggtgctggcgagctcaagcagttctctg 205

DB 470 AACCGGGGGCGGCGGAGCATAGCTCGGCGCGGCGGAGCTCAAGCAGTTCTCTCG 411

QY 206 gctggtcagaagcagcgcatactctcgaaaccttagttccgctgtacacagtgcc 265

DB 410 GCTGCTCAAGAAGCACGCTACTGCTGACCTTAGTTCGCTGTGTACGACAGTGGC 351

QY 266 gtgcttgatgcagaagtcacacaagcccccaaccagg 304

DB 350 GTGCTTGATGCAGAAGTCACACAGACCCGAAACAGG 312

RESULT 8

AV010798
LOCUS AV010798
DEFINITION Mus musculus 18-day embryo C57BL/6J Mus musculus CDNA
clone 1110029C24, mRNA sequence.
ACCESSION AV010798
NID 94787785
VERSION AV010798.1 GI:4787785
KEYWORDS EST
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 229)

Oy 836 ttgcaggccctcccacaatctctttaataataaaaggagtggttc 882
 |||||
Db 121 TTGCAGGCCCTCCCAAGAGTCCTCTTAAATAAATAAAGGAGTTGTTC 167

LOCUS	AA377893	247 bp	mRNA	EST	21-APR-1997
DEFINITION	EST505550	Synovial sarcoma	Homo sapiens	cdna 5' end,	mRNA sequence.
ACCESSION	AA377893				
NID	92030231				
VERSION	AA377893.1	GI:2030231			
KEYWORDS	EST.				
SOURCE	human.				

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1. (bases 1 to 247)

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodok, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.B., Saudex, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Korak, D.L., Kunsch, C., Wing, J., Li, H., Measner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Huang, J., Xu, C., Yu, C., Li, Y., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

TITLE Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE 96026280

TITLE Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE 96026280

Email: arkerlavetigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

```

/db_xref="taxon:9606"
/clone_lib="Synovial sarcoma"
/sex="female"
/tissue_type="synovial membrane"
/dev_stage="adult, 20 yrs"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
51 a 78 c 79 g 33 t 6 others

```

```

Query Match      11.5%   Score 108.2;   DB 32;   Length 247;
Best Local Similarity 84.4%;   Pred. NO. 2.2e-11;
Matches 130;   Conservative 0;   Mismatches 23;   Indels 1;   Gaps 1
QY 164 ccagctcgggcccgctgcggcgagctcaagcagttccttcggtcgctgcgaagaagcacq 223

```

Db 1 CNAAGCTCGGGCGGTGGCGGCCGA-NTCAAGCAGTTCCTGGCTGGCTCAAGAAGCAGC 59
 QY 224 cactactgctcgaaccttattccgcctgtacgacagtggtgctgtggatgcagaagt 283
 Db 60 CGTACTGCTCCACCTCAGCTTCGGCTCTAGACAGTGGCGGAGCCCTGGATNCAGAAGT 119
 QY 284 cacacaagaccgaaaccaggttaggaagtggg 317
 Db 120 CCACAAGACCGNAGNACCAAGCAGGAGGAGGG 153

RESULT 12 A1535068/c

LOCUS A1535068 234 bp mRNA EST 18-MAR-1999
 DEFINITION UI-R-C3-sx-d-03-0-UI.s1 UI-R-C3 Rattus norvegicus CDNA clone
 UI-R-C3-sx-d-03-0-UI 3', mRNA sequence.

ACCESSION A1535068

NID 9449203

VERSION A1535068.1 GI:4449203

KEYWORDS EST.

SOURCE Norway rat.

ORGANISM Rattus norvegicus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

AUTHORS Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

TITLE 1 (bases 1 to 234)

Normalization and subtraction: two approaches to facilitate gene

discovery

9704477

Genome Res. 6 (9), 791-806 (1996)

On May 18, 1998 this sequence version replaced gi:3136453.

Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa

451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. The sequence tag present in the cDNA between the NotI site

and the oligo-dT track served to identify it as a clone from the

normalized 18 day embryo library CDNA library preparation: M.B.

Soares Lab Clone Distribution: Clones will be available through

Research Genetics (www.resgen.com)

Seq primer: M13 Forward.

Location/Qualifiers

1. 234

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="UI-R-C3-sx-d-03-0-UI"

/clone_lib="UI-R-C3"

/dev_stage="adult"

/lab_host="DH10B (Life Technologies)"

/note="vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C3

library is a subtracted library of a series, ultimately

derived from a mixture of individually tagged normalized

libraries from rat placenta, adult lung, brain, liver,

kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day

embryos, after a series of subtractions to reduce the

representation of cDNAs from which ESTs had already been

generated. The following serially subtracted libraries

were generated in this process: UI-R-C3, UI-R-C2p,

UI-R-C1, UI-R-C0, UI-R-A1, UI-R-E1. The tag is a string of

3-5 nucleotides present between the Not I site and the

oligo-dT track which allows identification of the library

of origin of a clone within the mixture. The subtracted

library (UI-R-C3) was constructed as follows: PCR amplified

CDNA inserts from UI-R-C2p clones from which 3' ESTs had
 been derived was used as a driver in a hybridization with
 the UI-R-C2p library in the form of single-stranded
 circles. The remaining single-stranded circles (subtracted
 library) was purified by hydroxyapatite column
 chromatography, converted to double-stranded circles and
 electroporated into DH10B bacteria (Life Technologies) to
 generate the UI-R-C3 library. This procedure has been
 previously described (Bonaldo, Lennon and Soares, Genome
 Research. 6:791-806, 1996).

BASE COUNT 49 a 58 c 46 g 81 t

ORIGIN

Query Match 10.8% Score 101: DB 47: Length 234;

Best Local Similarity 74.08; Pred. No. 4.9e-10;

Matches 174; Conservative 0; Mismatches 45; Indels 16; Gaps 3;

QY 683 tggaggctcacctgaattggagccctctgtac---ctattctgggcaacaagaacctta 739

Db 234 TGGAGGCTCAGCTGAAGTGGAGACCATGTGTCTACATTGGGGCAATGAAGAACA 175

QY 740 ccattgagctggggcacaatgagctcccaacacacagctttgtccacatgatggtc 799

Db 174 ACCAGGGGCTGGGGCACAATGAGCTCCCAACACACAGCTTTGG-CCACATGATG 116

QY 800 acttggtatatacccccagctgggtgaagttg-----gggtattgcagggccctc 847

Db 115 CTTTGGATGATACCCCAATATGGGTGGAGTATGACAAAGGGTTATCGAGGCCCT 56

QY 848 ccaacaatcttttaataataaaggagttgttcaggtaaaaaaataaaaaa 902

Db 55 CCAAGAGCTCTTTGATATAATAAGAAAGAGTTGTTCAAAAAAATAAAAAA 1

RESULT 13

A1074921

LOCUS 404 bp mRNA EST 24-SEP-1998

DEFINITION OY0408.s1 Soares, senescent_fibroblasts_NBHSF Homo sapiens CDNA

clone IMAGE:1664847 3', mRNA sequence.

ACCESSION A1074921

NID 93401565

VERSION A1074921.1 GI:3401565

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On Jan 17, 1998 this sequence version replaced gi:1900484.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 761 Std Error: 0.00

Seq primer: -40m13 fwd. RT from Amersham

High quality sequence stop: 367.

Location/Qualifiers

1. 404

/organism="Homo sapiens"

/db_xref="taxon:9606"

/map="17q21: between D17S1321 and D17S1325; Xp11.4;

between AFMA2127G1 and DX6745"

/clone="IMAGE:1664847"

/clone_lib="Soares, senescent_fibroblasts_NBHSF"

/tissue_type="senescent fibroblast"

/lab_host="DH10B (ampicillin resistant)"

FEATURES source

/note="Vector: pT73D (Pharmacia) with a modified polylinker V-type: phagemid; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5], TGTTACCAATCTGAAGTGGGAGCGCCGCAATTTTTTTTTTTT 3', double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot - 5. Library constructed by Bento Soares and M.Fatima Bonaudo."

BASE COUNT 70 a 149 c 121 g 61 t 3 others

Query Match 10.7%; Score 100.2; DB 42; Length 404;
Best Local Similarity 86.0%; Pred. No. 7.5e-10;
Matches 111; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 176 cggtagtcgagcagctcagcagctcctcggctcggctcagcagcgcgcatactgctga 235

Db 196 CGCCGCGTGGAGACTCAAGCAGTCTCTGGCTGGCTCAAGAGCAGCGTACTGCTCCA 255

QY 236 acctagtttcgctgtagcagcagctcggctgctgtagcagcagcagcagcagcc 295

Db 256 ACCTCAGCTTCGGCTCTACGACCACTGGCGAGCTGGATGCAGAAAGTCGCACAGACCC 315

QY 296 gaacacagg 304

Db 316 GCAACACAGG 324

RESULT 14

W66776/c

LOCUS

DEFINITION

W66776 482 bp mRNA EST 14-JUN-1996

me17b11.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus cDNA

clone IMAGE:387741 5' similar to PIR:B38252 B38252 granulocyte

colony-stimulating factor receptor precursor ; mRNA sequence.

W66776

Q1375694

W66776.1 GI:1375694

EST.

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 482)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

The WashU-HHMI Mouse EST Project

Unpublished (1996)

On Apr 14, 1993 this sequence version replaced gi:785250.

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

/db_xref="taxon:10090"
/map="10 pter-cen"
/clone="IMAGE:387741"
/clone_lib="Soares mouse embryo NBME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5], TGTTACCAATCTGAAGTGGGAGCGCGCAATTTTTTTTTTTT 3', on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaudo."

BASE COUNT 96 a 138 c 147 g 101 t

Query Match 9.9%; Score 92.4; DB 26; Length 482;

Best Local Similarity 98.9%; Pred. No. 2.2e-08;

Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggcacgcttactctcgaagtgctgttaacccattcgggatctatgggtcgaaaaag 60

Db 103 GGCACGCTTACTCTCGTCCAAAGTGGTGTAAACCATTCGGGATCTATGGTTCGAAAAAG 44

QY 61 ggggaattcggagcagtgagtgagccacccaccc 94

Db 43 GCGGAATCTGGAGCGAGTGGGAGCACCACCCATCG 10

RESULT 15

AA270365

LOCUS

DEFINITION

AA270365 227 bp mRNA EST 26-MAR-1997

IMAGE:736103 5' mRNA sequence.

AA270365

Q1908728

AA270365.1 GI:1908728

EST.

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 227)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

The WashU-HHMI Mouse EST Project

Unpublished (1996)

On Sep 12, 1996 this sequence version replaced gi:1394722.

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:453151

Putative full length read

vector to vector length is 405

Seq primer: -28m13 rev2 ET from Amersham

FEATURES

source

High quality sequence stop: 177.

FEATURES
source

Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/map="Xp11.2: Xq23"
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/sex="unknown"
/tissue_type="fetus"
/dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
/note="Organ: whole fetus; Vector: p773D-Pac (Pharmacia)
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1st strand cDNA was primed with a Not I - oligo(dT) primer
(5' TGTTACCAATCTGAAGTGGAGGCGCGCTATTATTTTATTTT
3'), on total mouse RNA (provided by Minoru Ko, Wayne
State Univ.); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p773 vector.
Library went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 52 a 66 c 67 g 42 t
ORIGIN

Query Match 9.1%; Score 85; DB 30; Length 227;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 220 cagcgatactgtcgaaaccttagttccgcctgtacgaccagtgcgttgatgcag 279
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DB 1 CACGCATACGTGCGAACCTTAGTTCCGCTGTACGACCAGTGGCGTGTGGATGCAG 60
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QY 280 aagtcacacagaccgaaaccagg 304
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DB 61 AAGTCACACAGACCCGAACCCAGG 85

Search completed: September 28, 1999, 15:38:13
Job time: 3281 sec

A70388 Sequence 18

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AG"
BASE COUNT      167 a   274 c   225 g   168 t
ORIGIN

Query Match      100.0%; Score 834; DB 5; Length 834;
Best Local Similarity 100.0%; Pred. No. 1.4e-181;
Matches 834; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ggggccaacctgagggctctactggaacctcaatggtgcgcgcctgacctgagctg 120
Db 61 GGGGCCACCCTGAGGGGCTCTACTGGACCTCAATGTCGCGCCTGCGCCTCTGAGCTG 120
QY 121 tccgcctcttaacacctcacctgacctgacctgacctgaccttaatgggtccagg 180
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QY 181 cagcagtcaggagacaatctggtgtgtacgcccagagacggcagcattcttggctgcc 240
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Db 241 TGCCTCTATGTTGGCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGC 300
QY 301 atgaagatctcacgtgcctgagacacgggtgacacgggtgacacgggtgacacgggtgac 360
Db 301 ATGAGGATCTCAGTGCCTGACACCGGGTGCACCGGGGAGAGACATTTCTTACATACC 360
QY 361 aactactcctcaagtacagctgagctgagctgagctgagctgagctgagctgagctgagct 420
Db 361 AACTACTCCTCAAGTACAGCTGAGGTGTACGGTTCAGGATAACACATGTGAGGAGTAC 420
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RESULT 2

A70382 A70382 1629 bp DNA PAT 07-MAY-1999

LOCUS Sequence 12 from Patent WO9811225.

DEFINITION A70382

ACCESSION A70382

NID 94774663

VERSION A70382.1 GI:4774663

KEYWORDS

SOURCE unidentified.

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1629)

AUTHORS Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S., Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and Kikuchi, Y.

TITLE A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME

JOURNAL Patent: WO 9811225-A 19-MAR-1998;

NICOLA NIGOS ANTONY (AU)

FEATURES

Location/Qualifiers

source 1..1629

/organism="unidentified"

/db_xref="taxon:32644"

BASE COUNT 336 a 541 c 453 g 299 t

ORIGIN

Query Match 99.6%; Score 830.8; DB 5; Length 1629;

Best Local Similarity 99.8%; Pred. No. 7e-181;

Matches 832; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 274 CCCACCCTTCTCATCGGCTCTCCCTGCAAGCTACCTGCTCTATACATGAGACACACT 333

QY 61 ggggccaacctgagggctctactggaacctcaatggtgcgcgcctgacctgagctg 120

Db 334 GGGGCCACCCTGAGGGGCTCTACTGGACCTTCAATGTCGCGCCTGCGCCTTGCCTTGCAGTG 393

QY 121 tccgcctcttaacacctcacctcctccctgacctgacctgaccttaatgggtccagg 180

Db 394 TCCCGCCTCTTAACACCTTCCACCTGCGCCTGCGCCTGCGCCTGCGCTTAATGGTCCAGG 453

QY 181 cagcagtcaggagacaatctggtgtgtacgcccagagacggcagcattcttgcctgctcc 240

Db 454 CAGCAGTCAGGAGACAATCTGGTGTGTACGCGCCGAGACGGCAGCATTTCTGCTGCTCC 513

QY 241 tgcctctatgttggttgcctcctgagagacctttaaactcagctgctggttcccggaac 300

Db 514 TGCCTCTATGTTGGCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGC 573

QY 301 atgaagatctcacgtgcctgagacacgggtgacacgggtgacacgggtgacacattcttataacc 360

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QY 421 cacaactgtggggcccaactcatgccatatacccaaggacctgaccttcttcaactccctat 480

Db 694 CACACTGTGGGGCCCACTCATGCCATATCCCAAGGACCTGCGCCTCTTCACTCCCTAT 753

QY 481 gagatctgggtggaagcccaactcgcctaggtcagcaagatctgcttccctcacactg 540

Db 754 GAGATCTGGGTGGAGCCCACTAGCTAGGCTCAGCAAGATCTGATGTCTCTCACACTG 813

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Qy	601	ggcttgaggaccagctgagtgtgcgtgggtctccaccaccagctctcaaggattctctc	660
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Qy	661	ttcceaagccaagtaccagatccgtaccgctgagggagacagctggactggaaagtggtg	720
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Qy	721	gatcagctcagcaaccaagacctctcgtctcggcggtgaagcccgccaccgctttac	780
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DEFINITION	Sequence 14 from Patent WO9811225.		PAT
ACCESSION	A70384		
NID	94774664		
VERSION	A70384.1	GI:4774664	
KEYWORDS			
SOURCE	unidentified.		
ORGANISM	unidentified.		
REFERENCE	1 (bases 1 to 1673)		
AUTHORS	Nicola, N.A.; Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S., Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and Kikuchi, Y.		
TITLE	A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME		
JOURNAL	Patent: WO 9811225-A 19-MAR-1998;		
FEATURES	NICOLA NICOS ANTONY (AU)		
source	Location/Qualifiers		
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BASE COUNT	344 a 550 c 474 g 305 t		
ORIGIN			
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Best Local Similarity 99.8%; Pred. No. 7e-181;			
Matches 832; Conservative 0; Mismatches 2; Indels 0; Gaps			
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Qy	61	ggggccaccgctgaggggtctactggaccctcaatggctgcgcgcctgcctctgagctg	120
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Qy	301	atgaaggaattcacgtgccgctggacacccgggtgcacacggggagacattcttacatacc	360
Db	575	atgaaggaattcacgtgccgctggacacccgggtgcacacggggagacattcttacatacc	634
Qy	361	aactactcctcaagtacaagctgaggtggtacggttcaggataaacacatgtagagtagtac	420

DB	635	AACTACTCCCTCAAGTACAAAGCTGAGGTGGTACCGGTGAGGATAACACATGTGAGGAGTAC	694
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DB	695	CACACTGTGGGCGCTCACTCATGCGCATATCCCCAAGACCTGGCCCTTTCACCTCCCTAT	754
QY	481	gagatctgtgggtggaagccaccatctgcctaggctcagcaagatctgatgtctctcacactg	540
DB	755	GAGATCTGGTGGTGAAGCACCACCAATCGGCTAGGCTCAGCAAGATCTGATGTCTTCACACTG	814
QY	541	gatctctgacgtggtgaccacagagccccccccccccacacgtgcaactgagccggttggg	600
DB	815	GATCTCTGGACGTGGTGAACACAGGACCCGCCACCCGACGTGCACGTGAGCGCGTTGGG	874
QY	601	ggcctggaggaccagctgagtgtgctggtctcaccaccagctctcaaggatttcctc	660
DB	875	GGCCTGGAGGACCAAGCTGAGTGGCTGGGTCTCACCCACAGCTCTCAAGGATTTCCTC	934
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QY	721	gatgactcagcaaccagacactcctgcgtctgcgggctgaagccccggcacctgttac	780
DB	995	GATGACTCAACCAACCAAGACCTCTGCGGTCTCGGGGCTGAAGCCGCGCACCGTTTAC	1054
QY	781	ttcgtccaaatggtgtgaaccattcggatctatggttcgaaaaagcggga	834
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DEFINITION	Sequence 22 from Patent WO9811225.		PAT
ACCESSION	A70392		07-MAY-1999
NID	94774670		
KEYWORDS	A70392.1	GI:4774670	
SOURCE	unidentified.		
ORGANISM	unidentified.		
REFERENCE	1 (bases 1 to 1930)		
AUTHORS	Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S., Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and Kikuchi, Y.		
TITLE	A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME		
JOURNAL	Patent: WO 9811225-A 19-MAR-1998;		
FEATURES	Location/Qualifiers		
source	1. 1930		
BASE COUNT	375 a 523 c 561 g 371 t		
ORIGIN			
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Best Local Similarity	99.8%;	Pred. No. 6.9e-181;	
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QY	61	ggggccacgcgtgaggggtctactggaacctcaatggtcgcgcctgcctctgagctg	120
DB	335	GGGGCCACCGCTGAGGGGCTCTACTGGACCCCTCAATGTCGCGGCTGCCCTCTGAGCTG	394
QY	121	tccgcctctctaaacacctccaccctggccctggccctggcttaacctaatgggtccagg	180
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Query Match	99.6%	Score 830.8;	DB 5;	Length 1930;
Best Local Similarity	99.8%;	Pred. No. 6.9e-181;		
Matches 832;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0

Query Match	99.6%;	Score 830.8;	DB 5;	Length 1673;
Best Local Similarity	99.8%;	Pred. NO. 7e-181;		
Matches 832;	Conservative	0;	Mismatches 2;	Indels 0;
			Gaps	0;

1 (bases 1 to 1930)
 Nicole, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S.,
 Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and
 Kikuchi, Y.
 A NOVEL HAEMOPHAGOCYTIC RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
 TITLE
 JOURNAL
 Patent: WO 9811225-A-19-MAR-1999;

FEATURES	Location/Qualifiers
source	1. 1930

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CASE COUNT
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/organism="unidentified"
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RESULT 5
AF059293 1716 bp mRNA PRI 02-AUG-1998
LOCUS Homo sapiens cytokine-like factor-1 precursor (CLF-1) mRNA,
DEFINITION complete cds.
ACCESSION AF059293
NID 93372626
VERSION AF059293.1 GI:3372626
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1716)
AUTHORS Elson,G.C.A., Graber,P., Losberger,P., Herren,S., Gretener,D.,
Menoud,L.N., Wells,T.N.C., Kosco-Vilbois,M.H. and Gauchat,J.F.
CLF-1, a Novel Soluble Protein Shares Homology With Members of the
Cytokine Type-1 Receptor Family
J. Immunol. (1998) In press
REFERENCE 2 (bases 1 to 1716)
AUTHORS Elson,G.C.A., Graber,P., Losberger,P., Herren,S., Gretener,D.,
Menoud,L.N., Wells,T.N.C., Kosco-Vilbois,M.H. and Gauchat,J.F.
Direct Submission
Submitted (14-APR-1998) Dept. of Immunology, SeroPharmaceutical
Research Institute, 14, Chemin des Aulx, Plan-les-Ouates, GE 1228,
Switzerland
FEATURES
Location/Qualifiers
1..1716

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Best Local Similarity 87.4%; Pred. No. 6.2e-143;
Matches 728; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

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Qy 61 ggggcccacgctgaggggctctactggaccctcaatgctgcgcgctgcccctctagctg 120
Db 320 GGAGCCACCGCGAGGGCTCTACTGGACCCTCAACGGGCGCGCTGCCCCCTGAGCTC 379
Qy 121 tcccgcctcttaacacacccctgcccctggccctggcttaacatttaattggtccagg 180
Db 380 TCCCCTGTACTCAACGCTCCACCTTGGCTGTGGCCCTGGCCCACTCAATGGGTCAGG 439
Qy 181 cagcagtcagagagacaatctggtgtgtcagcccgagacggcagcattctggtgctcc 240
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Qy 241 tgcctctatgttggtgtgccccctgagaagccctttaacatacagctgctggtcccggaac 300
Db 500 TGCTCTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 559
Qy 301 atgaagagatcagctgctggtggtggtggtggtggtggtggtggtggtggtggtggtggt 360
Db 560 ATGAAGGACTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 619
Qy 361 aactactccctcaagatacagctgagtggtggtggtggtggtggtggtggtggtggtggt 420
Db 620 AACTACTCCCTCAAGTACAGCTTATGGTGTGGCCAGGAGCAACATGTGAGGAGTAC 679
Qy 421 cacactgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 480
Db 680 CACACAGTGGGGGCCCCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 739
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RESULT 10
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LOCUS Human DNA from chromosome 19 specific cosmid R30292, genomic
DEFINITION sequence, complete sequence.
ACCESSION AC003112
NID 92636669
VERSION AC003112.1 GI:2636669
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 40668)
AUTHORS Lamerdin,J.E., McCready,P.M., Adamson,A.W., Burkhardt-Schultz,K.,
Gordon,L., Christensen,M., Kyle,A., Ramirez,M., Stilwagen,S.,
Garnes,J., Dangnanan,L., Bruce,R., Quan,G., Montgomery,M., Ow,D.,
Kobayashi,A., Olsen,A.O. and Carrano,A.V.
TITLE Sequence analysis of an -1 Mb region containing the MEF2B gene in
19p12
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 40668)
AUTHORS Lamerdin,J.E.
DIRECT SUBMISSION
TITLE Submitted (21-NOV-1997) Human Genome Center, Lawrence Livermore
NATIONAL LABORATORY, 7000 East Ave., Livermore, CA 94551, USA
FEATURES
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/notes="LL19NC03 cosmid library constructed at LLNL from
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frame: 1, quality: good, score: 62.000"
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complement(7505..7783)
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8951..9254
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9358..9535
repeat_region /rpt_family="LTR12"
complement(9445..9505)
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frame: 1, quality: good, score: 63.000"
complement(9629..9672)
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frame: 1, quality: excellent, score: 75.000"
complement(9928..10123)
repeat_region /rpt_family="Alu"
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heart NBHH19W Homo sapiens cDNA clone 377018 5' (1..138);

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96% identity.--Other overlapping matches:--(10435..10548)
DDB similarity to AA136115 zk90b04.r1 Soares pregnant
uterus NBHPU Homo sapiens cDNA clone 490063 5' (1..110);
93% identity.--(10466..10548) DDB similarity to AA452628
zx33f04.r1 Soares total fetus NB2HF8 9w Homo sapiens cDNA
clone 788287 5' (1..82); 95% identity.--(10486..10548) DDB
similarity to AA009412 ze82h02.r1 Soares fetal heart
NBHH19W Homo sapiens cDNA clone 365523 5' (1..61); 97%
identity.--
10643..10725
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identity.--DDB similarity to AA136115 zk90b04.r1 Soares
pregnant uterus NBHPU Homo sapiens cDNA clone 490063 5'
(111..192); 99% identity.--DDB similarity to AA452628
zx33f04.r1 Soares total fetus NB2HF8 9w Homo sapiens cDNA
clone 788287 5' (83..165); 100% identity.--DDB similarity
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sapiens cDNA clone 365523 5' (62..144); 100% identity.--
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ze82h02.r1 Soares fetal heart NBHH19W Homo sapiens cDNA
clone 365523 5' (145..346); 96% identity.--(11121..11331)
DDB similarity to AA009693 ze82h02.s1 Soares fetal heart
NBHH19W Homo sapiens cDNA clone 365523 3' (429..307); 95%
identity.--(11127..11246) DDB similarity to AA047548
zf15e02.r1 Soares fetal heart NBHH19W Homo sapiens cDNA
clone 377018 5' (222..341); 97% identity.--(11061..11331)
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quality: good, score: 73.000--(11061..11209) DDB
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NB2HF8 9w Homo sapiens cDNA clone 788287 5' (167..313);
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clone 365523 5' (347..427); 94% identity.--DDB similarity
to AA009693 ze82h02.s1 Soares fetal heart NBHH19W Homo
sapiens cDNA clone 365523 3' (306..228); 99%
identity.--DDB similarity to AA450010 zx33f04.s1 Soares
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frame: 2, quality: good, score: 61.000--Other overlapping
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clone 365523 5' (428..496); 97% identity.--(13756..13984)
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NBHH19W Homo sapiens cDNA clone 365523 3' (227..1); 98%
identity.--(13756..13984) DDB similarity to AA450010
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complement(14100..14672)
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to W37175 zb21a02.r1 Soares fetal lung NBHH19W Homo
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identity.--(15227..14885) DDS similarity to AA121532
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 clone 490004 3' (342..1); 99% identity.--(15227..14885)
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 uterus NBHPU Homo sapiens cDNA clone 490004 5' (126..467);
 99% identity.--(15227..14897) DDS similarity to W46603
 zc32h10.r1 Soares senescent fibroblasts NBHSF Homo sapiens
 cDNA clone 324067 5' (328..1); 98%
 identity.--(15227..15088) DDS similarity to W46604
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 cDNA clone 324067 3' (322..465); 96% identity."
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 clone 490004 5' (77..125); 90% identity.--(15735..15713)
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 fibroblasts NBHSF Homo sapiens cDNA clone 324067 5'
 (351..329); 100% identity.--(15735..15713) DDS similarity
 to W46604 zc32h10.s1 Soares senescent fibroblasts NBHSF
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 (157..1); 82% identity.--(18438..18406) DDS similarity to
 AA049280 m145d02.r1 Soares mouse embryo NBME13 5' 14.5 Mus
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 NBME13 5' 14.5 Mus musculus cDNA clone 387741 5' similar to
 PIR:B38252 B38252 granulocyte colony-stimulating factor
 receptor precursor (316..158); 92% identity.--DDS
 similarity to AA049280 m145d02.r1 Soares mouse embryo
 NBME13 5' 14.5 Mus musculus cDNA clone 479043 5' similar to
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 PRECURSOR (274..431); 93% identity.--"

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 Db 21408 GGAGCCACCGCCGAGGGCCCTCTACTGGACCCCTAACGGGGCCGCTGCCCTGAGCTC 21349
 Qy 121 tccgcctcttaacacctccacccctggtccctggtccctggtacacctaagtggctcagg 180
 Db 21348 TCCCGTGTACTACACGCTCCACCTTGGCTCTGGCCCTGGCCACCTCATGGGTCAGG 21289

Qy 181 cagcagtcagagacaactctgtgtgtcacaccgagacgacgacgacattctgctgctcc 240
 Db 21288 CAGCGGTGGGGAGAACCTGTGTGTGACGCCCGGTGACGGCAGCATCTTGCTGCTCC 21229
 Qy 241 tgcctctatgtttggc 255
 Db 21228 TGCTCTATGTGGC 21214
 RESULT 11
 A70386
 LOCUS A70386 938 bp DNA PAT 07-MAY-1999
 DEFINITION Sequence 16 from Patent WO9811225.
 ACCESSION A70386
 NID 94774665
 VERSION A70386.1 GI:4774665
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 unclassified.
 REFERENCE 1 (bases 1 to 938)
 AUTHORS Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
 Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
 Kikuchi,Y.
 TITLE A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
 JOURNAL Patent: WO 9811225-A 19-MAR-1998;
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 Best Local Similarity 100.0%; Pred. No. 8.3e-06;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 769 ggcacgtttacttgcctcaagtgcgttttaaccattcgggatctatggtcgagaaag 828
 Db 1 GGCACGTTTACTTCTGCAAGTGCCTTGAACCCATCGGATCTATGGTTCGAAAAAG 60
 Qy 829 gcggga 834
 Db 61 GCGGGA 66
 RESULT 12
 A70386
 LOCUS A70386 2635 bp mRNA MAM 15-SEP-1989
 DEFINITION Rabbit prolactin receptor 2 mRNA, complete cds.
 ACCESSION J04510
 NID 9165669
 VERSION J04510.1 GI:165669
 KEYWORDS
 SOURCE Rabbit (14-day pregnant) mammary gland, cDNA to mRNA, clones
 PRLR-2(1,4).
 ORGANISM Oryctolagus cuniculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 REFERENCE 1 (bases 1 to 2635)

AUTHORS Edery, M., Jolicœur, C., Levi-Meyrueis, C., Dusanter-Fourt, I., Petridou, B., Boutin, J.-M., Lesueur, L., Kelly, P.A. and Djiane, J.
TITLE Identification and sequence analysis of a second form of prolactin receptor by molecular cloning of complementary DNA from rabbit mammary gland
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116 (1989)
MEDLINE 89184578
COMMENT Draft entry and computer-readable sequence for [1] kindly provided by J. Djiane, 14-MAR-1989.
FEATURES
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1. 2635
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Matches 165; Conservative 0; Mismatches 153; Indels 9; Gaps 2;
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Db 555 CCTCTGGAACACCTTTCATCTCAATGCGCTCTCCTGAGAGGAACATTCACCTGC 614
QY 319 cgcctggacacgggtgcacacggggagacattcttatacacaactactcctcctcaagtac 378
Db 615 TGGTGGAGGCGCTGGAGCAGACGG-----AGGACTTCTACCAATATACACACTGACTTAC 668
QY 379 aagctgaggtggtacggtccaggataacacacatgtaggagtagcacacactgtggggcccccac 438
Db 669 CACAAGGAAGGAGAAACAATCATTCTAGTAGTGTCCAGACTACAAGCGGGTGGTCCCAAC 728
QY 439 tcattgcca---tatcccaaggacgctggccctcttcaacctcctatgagatctgggtgaa 495
Db 729 TCCGTGTACTTTAGCAAGAACACACCTCCATATGGAGGATATACATCATCAGATGNAAT 788
QY 496 gccaccaatgccttagctcgaagaatctgtagtctctcactcagtgatgctcctggagtg 555
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QY 556 gtgaccacgacccccaccacccagctg 582
Db 849 GTTGAACACAGACCTCTCTGTGAACCTG 875
RESULT 13
GGU37273
LOCUS GGU37273 1531 bp mRNA VRT 08-JAN-1997
DEFINITION Gallus gallus winged helix protein CWH-2 mRNA, complete cds.
ACCESSION U37273
NID 91766074

U37273.1 GI:1766074
KEYWORDS chicken.
SOURCE Gallus gallus
ORGANISM Gallus gallus
REFERENCE 1 (bases 1 to 1531)
AUTHORS Freyaldenhoven, B.S., Freyaldenhoven, M.P., Iacovoni, J.S. and Vogt, P.K.
TITLE Aberrant cell growth induced by avian winged helix proteins
JOURNAL Cancer Res. 57 (1), 123-129 (1997)
MEDLINE 97141794
REFERENCE 2 (bases 1 to 1531)
AUTHORS Freyaldenhoven, B.S. and Freyaldenhoven, M.P.
TITLE Direct Submission
JOURNAL Submitted (29-SEP-1995) Bettina S. Freyaldenhoven, Department of Molecular and Experimental Medicine, SBR-7, Scripps Research Institute, 10666 North Torrey Pines Road, La Jolla, CA 92037, USA
FEATURES
source Location/Qualifiers
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QY 690 cgtggagacagcgtggaaggtgggtggatgacgtcagcaaccagacacctctctccg 749
Db 61 CGTCTCGACCCCAACACTTGGGAGTGGCCCTATTAAAGCGAGCAGACTACTACCG 120
QY 750 tctcgcggcctgaagcccgccacgcgtttactctgctcgaagtcggttaacccattcgg 809
Db 121 GACGGCGGACGCTACGGCGGCATGGGCAACCCCATGAGCGTGTATTACGCGCACCGCGCA 180
QY 810 gatctatggttcgaagaagcggga 834
Db 181 GCAGTACGCGCGGCATGGGCGCA 205
RESULT 14
GGU95823
LOCUS GGU95823 1849 bp mRNA VRT 06-MAY-1997
DEFINITION Gallus gallus winged helix transcriptional factor MFH-1 mRNA, complete cds.
ACCESSION U95823
NID 92072323
VERSION U95823.1 GI:2072323
KEYWORDS chicken.

ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus;
REFERENCE 1 (bases 1 to 1849)
AUTHORS Arase, Y., Koseki, H. and Miura, N.
TITLE Winged helix transcriptional factor MFH-1 is required for the
generation of medial structures of the vertebrae and the
neurocranium
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1849)
AUTHORS Koseki, H.
TITLE Direct Submission
JOURNAL Submitted (28-MAR-1997) Molecular Immunology, School of Medicine,
Chiba University, 1-8-1, Inohana, Chuo-ku, Chiba 20, Japan
FEATURES
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1. .1849
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BASE COUNT 416 a 609 c 521 g 303 t
ORIGIN

Query Match 5.28; Score 43.4; DB 4; Length 1849;
Best Local Similarity 50.7%; Pred. No. 1.2;
Matches 104; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

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Qy 690 cgtgagacagcgtggtgactgaagtggtggtggtggtggtggtggtggtggtg 749
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Qy 810 gatctatgggtgtaaaaggcg99ga 834
Db 445 GCAGTACGCGCGCGCATGGCGCA 469

RESULT 15
LOCUS CLU07694 2713 bp mRNA VRT 11-AUG-1994
DEFINITION Columba livia prolactin receptor mRNA, complete cds.
ACCESSION U07694
NID 9466381
VERSION U07694.1 GI:466381
KEYWORDS domestic pigeon.
ORGANISM Columba livia
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Columbiformes; Columbidae; Columba.
REFERENCE 1 (bases 1 to 2713)
AUTHORS Chen, X. and Horseman, N.D.

TITLE Cloning, expression, and mutational analysis of the pigeon
prolactin receptor
JOURNAL Endocrinology 135 (1), 269-276 (1994)
MEDLINE 94283267
REFERENCE 2 (bases 1 to 2713)
AUTHORS Chen, X.
TITLE Direct Submission
JOURNAL Submitted (14-MAR-1994) Xiaojuan Chen, Physiology & Biophysics,
University of Cincinnati Medical College, 231 Bethesda Ave.,
Cincinnati, OH 45267, USA
FEATURES
Location/Qualifiers
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/db_xref="taxon:8932"
/clone_lib="pCLR"
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1. .178
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179. .250
sig_peptide
mat_peptide 251. .2688
/product="prolactin receptor"
2672. .2713
BASE COUNT 907 a 554 c 575 g 677 t
ORIGIN

Query Match 5.18; Score 42.2; DB 4; Length 2713;
Best Local Similarity 49.8%; Pred. No. 2.2;
Matches 166; Conservative 0; Mismatches 158; Indels 9; Gaps 2;

Qy 243 cctctatgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 302
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Qy 303 gaaggtatctcaagtcggtggtggtggtggtggtggtggtggtggtggtggt 362
Db 913 GGAACATTTACTTGTGTTGGAACCTGTTTCAGATGG-----AGGACATCT 966
Qy 363 ctactccctcaagtacagtcggtggtggtggtggtggtggtggtggtggtggtggt 422
Db 967 CTACACTTGTCTTTACAGCAAGAAAGAGAGAGAGAGATTTATGAGTGTCCAG 1026
Qy 423 cactgtggggcccaactcagtcgcatatcccaaggaagcctggccctcttc 479
Db 1027 AACTGCAGGCCCAATTCCTACTCTCGATAAAGACACACCTCTTCTTGAC 1086
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Db 1087 CAATATAACTGTGAAGCACTAATGAATGGAAGTGAAGTGAAGTGAAGTGA 1146

Oy 540 ggatgtcctggacgtggtgaccacggacccccc 572
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Db 1147 GGATGTGACTTACATAGTACAGACAGATCCTCC 1179

Search completed: September 28, 1999, 16:39:55
Job time: 6982 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 28, 1999, 16:45:44 ; Search time 303.81 Seconds
(without alignments)
586.811 Million cell updates/sec

Title: US-09-037-657-18

Perfect score: 834
Sequence: 1 cccacccttctcatcggtct.....atgggtcgaaaaagcgcgga.834

Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	834	100.0	834	1	V27143	Nucleotide sequence
2	830.8	99.6	1930	1	V27158	Unspliced murine N
3	830.8	99.6	1829	1	V27140	Novel haemopoietin
4	830.8	99.6	1673	1	V27141	Novel haemopoietin
5	826	99.0	1656	1	V41688	Nucleotide sequence
6	760.4	91.2	1724	1	V70896	CDNA encoding rat
7	666.6	79.9	1813	1	V70895	CDNA encoding an a
8	665	79.7	1579	1	V41689	Nucleotide sequence
9	665	79.7	1890	1	V70894	CDNA encoding huma
10	598.8	71.8	1391	1	V27144	Nucleotide sequence
11	456	54.7	560	1	V27159	PCR product for hu
12	254.4	30.5	11832	1	V27148	Nucleotide sequence
13	254.4	30.5	6563	1	V27145	Nucleotide sequence
14	128.8	15.4	259	1	V70897	Expressed sequence
15	81.2	9.7	210	1	V70899	Expressed sequence
16	66	7.9	938	1	V27142	Novel haemopoietin
17	40.6	4.9	2723	1	O10550	Novel haemopoietin
18	38.6	4.6	2251	1	T11741	Human prolactin re
19	36.4	4.4	114955	1	X53491	Human,adenosine Al
20	35.4	4.2	423	1	T00690	Tilapia prolactin
21	35.2	4.2	2934	1	V41922	Type II topoisomer
22	35	4.2	4696	1	T13330	Nucleotide sequence
23	34.6	4.1	15079	1	O91580	Rat type I insulin
24	34.4	4.1	2568	1	T14891	S. clavuligerus cl
25	34	4.1	15864	1	T09312	DNA encoding phosph
26	34	4.1	15864	1	T51224	Mycobacteriophage
27	34	4.1	15864	1	T66130	Nhei-G/Spel fragme
28	34	4.1	15864	1	T70492	Mycobacteriophage
29	33.4	4.0	1018	1	T02326	Mycobacteriophage
30	33.4	4.0	1018	1	T87014	Human cardiac hype
31	33.2	4.0	8169	1	V28609	Human cardiotoxophi
32	33.2	4.0	49272	1	V35000	Actinomadura hibis
33	33	4.0	17955	1	V55642	Mycobacteriophage
34	32.8	3.9	5721	1	O06613	Actinoplanes sp. a
35	32.8	3.9	6381	1	N91167	Adenyl cyclase gen
36	32.6	3.9	4281	1	Q53471	Sequence encoding
37	32.6	3.9	3147	1	T86704	elk cDNA, Expressi
38	32.6	3.9	1851	1	V71205	DNA encoding therm
39	32.6	3.9	1448	1	X19959	DNA encoding ester
40	32.4	3.9	3007	1	O68842	Human Tango-83 5'-
41	32.4	3.9	44377	1	T78508	Plant blight-speci
42	32.4	3.9	44377	1	T78508	Platenolide syntha
43	32.2	3.9	43734	1	O80414	Platenolide syntha
44	32.2	3.9	3234	1	Q30999	Notc clone hn3k f

44	32.2	3105	1	T07308	Receptor tyrosine
45	32.2	3105	1	T84528	Mouse Nuk tyrosine

ALIGNMENTS

RESULT 1

V27143
ID V27143 standard; cDNA; 834 BP.
AC V27143;
DT 29-SEP-1998 (first entry)
DE Nucleotide sequence of products generated by 5N race of brain cDNA.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening; ss;
KW mouse.
OS Mus sp.
FH Key
FT CDS
FT
FT
FT
FT
PN WO9811225-A2.
PD 19-MAR-1998.
PP 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIE-) DZIEGLEWSKA H E.
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
PI Zhang J;
DR WPI: 98-260970/23.
DR P-PSDB; W55014.
PT
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PT Claim 7; Page 93-95; 182pp; English.
PS The nucleotide sequence was generated by a 5N RACE of brain cDNA using
PS NR6 specific primers. NR6 is a novel haemopoietin receptor (HR).
CC Interaction between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and its
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SQ Sequence 834 BP; 167 A; 274 C; 225 G; 168 T.

Query Match	100.0%	Score 834	DB 1	Length 834	
Best Local Similarity	100.0%	Pred. No. 3.9e+209			
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DB	1	CCACACCTTCTCATCGCTGCCCTCCCTGCAAGCTAGCTGCTCTATACATGGAGACACACT	60		
QY	61	ggggccacgcctgaggggctctactggaccctcaatggtgcgcgcctgccctctcgaagctg	120		
DB	61	GGGGCCACCGCTGAGGGGCTCTACTGGACCCCTCAATGTTGCGCGCTGCCCTCTGAGCTG	120		
QY	121	tccgcgctcctctaaacacctcccacccctggccctggccctgcttaacctaaatgggtccagg	180		
DB	121	TCCGCGCTCCTTAACACACTTCCACCCCTGCCCTTGGCCCTTGGCTTAACCTTAATGGGTCCAGG	180		
QY	181	cagcagctcaggagacaactgtgtgtgtcacgcgcgagacgcgcagcatctcgtcggctccc	240		
DB	181	CAGCAGTCAAGGAGACAANTGTGTGTGTCTACGCCCGCAGCGCAGCATCTCTGGCTGGCTCC	240		
QY	241	tgcctctatgttggcttggccccctgagaagccctttaacatcagctgctgtgcgccggaac	300		
DB	241	TGCTCTATGTGTGGCTTGCCCTCTCAGAAAGCCCTTTAATCATCACTGCTGTGCTCCGCGNAC	300		


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PN      W09811225-A2.
PD      19-MAR-1998.
PF      11-SEP-1997; G02479.
PR      11-SEP-1996; AU-002246.
PA      (AMRA-) AMRAD OPERATIONS PTY LTD.
PA      (DZIE/) DZIEGLEWSKA H E.
PI      Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI      Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
PI      Zhang J;
DR      WPI; 98-260970/23.
DR      P-PSDB; W55011.
PT      New isolated haemopoietin receptor - used for developing products
PT      for modulating proliferation, differentiation and survival of cells,
PT      e.g. neuronal cells
PS      Claim 4; Page 77-81; 182pp; English.
CC      The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6.
CC      Interaction between the novel HR and a ligand facilitates proliferation,
CC      differentiation and survival of a wide variety of cells. The HR and its
CC      derivatives can be used for modulating the activity of the receptors e.g.
CC      to regulate development, maintenance or regeneration in an array of
CC      different cells and tissues in vitro and in vivo. They can be present in
CC      therapeutics used for modulating neuronal proliferation, differentiation
CC      and survival. The products can also be used for detection and diagnosis,
CC      e.g. for cancers or predisposition to cancers, or for drug screening.
SQ      Sequence 1629 BP; 336 A; 541 C; 453 G; 299 T;

Query Match          99.6%; Score 830.8; DB 1; Length 1629;
Best Local Similarity 99.8%; Pred. No. 3.2e-208;
Matches 832; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 cccaccccttctcagctcgcctccctcgaagctacgtcctctctatcatgagacacact 60
DB      274 cccaccccttctcagctcgcctccctcgaagctacgtcctctatcatgagacacact 333
QY      61 gggggcacgcgtgaggggctctactgagaccctcaatggtcgccgctgaccttgagctg 120
DB      334 gggggcacgcgtgaggggctctactgagaccctcaatggtcgccgctgaccttgagctg 393
QY      121 tcccgctccttaacacctccacctggccctggccctggccctggccctggccctggccctg 180
DB      394 tcccgctccttaacacctccacctggccctggccctggccctggccctggccctggccctg 393
QY      181 cagcagctcaggagacaatctggtgtggtgcagcccgagacgagcagcattctggctgctcc 240
DB      454 cagcagctcaggagacaatctggtgtggtgcagcccgagacgagcagcattctggctgctcc 513
QY      241 tgcctctatgttggtgctgccccctgagaagccctttaacatcagctgctggttcccggaac 300
DB      514 tgcctctatgttggtgctgccccctgagaagccctttaacatcagctgctggttcccggaac 573
QY      301 atgaagatctcagtcgcgtgagacacacgggtgacacggggagagacattcttataacc 360
DB      574 atgaagatctcagtcgcgtgagacacacgggtgacacggggagagacattcttataacc 633
QY      361 aactactcctcaagtacacagctgaggtggtacggtcagagataacacatgtgagaggtac 420
DB      634 aactactcctcaagtacacagctgaggtggtacggtcagagataacacatgtgagaggtac 693
QY      421 cacactgtggggcccaactcatgccataatcccccaaggacctggccctcttcaactccctat 480
DB      694 cacactgtggggcccaactcatgccataatcccccaaggacctggccctcttcaactccctat 753
QY      481 gagactgtgggtggaagcccaactcagcttagctcagcaagatctgtatctcctcacactg 540
DB      754 gagactgtgggtggaagcccaactcagcttagctcagcaagatctgtatctcctcacactg 813
QY      541 gatgtccttgagcgtggtgacacagacaccccccaccccgacgtgacagcgtgagcgttggg 600
DB      814 gatgtccttgagcgtggtgacacagacaccccccaccccgacgtgacagcgtgagcgttggg 873

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QY      601 ggcctggaggaccagctgagtgctgctgggtctcacaccagctctcaaggatttcctc 660
DB      874 ggcctggaggaccagctgagtgctgctgggtctcacaccagctctcaaggatttcctc 933
QY      661 ttcaagcccaagtaccagatccgcgtacccggtgagacagcgtggactggaagtgtgtg 720
DB      934 ttcaagcccaagtaccagatccgcgtacccggtgagacagcgtggactggaagtgtgtg 993
QY      721 gatcagctcagcaaccagacctctgcgtctcggggctggaagcccgccacgcgtttac 780
DB      994 gatcagctcagcaaccagacctctgcgtctcggggctggaagcccgccacgcgtttac 1053
QY      781 ttctccaagtgcgtgttaaccattcggtatctatggctcgaaaaagcgggga 834
DB      1054 ttctccaagtgcgtgttaaccattcggtatctatggctcgaaaaagcgggga 1107

RESULT 4
V27141
ID      V27141 standard; cDNA; 1673 BP.
AC      V27141;
DE      25-SEP-1998 (first entry)
DE      Novel haemopoietin receptor NR6.2 gene.
KW      Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW      cell survival; therapeutic; neuronal proliferation; drug screening; ss;
KW      Mouse.
OS      Mus sp.
FH      Key
FT      CDS
FT      1..1278
FT      /*tag= a
FT      /product= "Haemopoietin receptor NR6.2"
W09811225-A2.
PD      19-MAR-1998.
PF      11-SEP-1997; G02479.
PR      11-SEP-1996; AU-002246.
PA      (AMRA-) AMRAD OPERATIONS PTY LTD.
PA      (DZIE/) DZIEGLEWSKA H E.
PI      Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI      Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
PI      Zhang J;
DR      WPI; 98-260970/23.
DR      P-PSDB; W55012.
PT      New isolated haemopoietin receptor - used for developing products
PT      for modulating proliferation, differentiation and survival of cells,
PT      e.g. neuronal cells
PS      Claim 5; Page 84-87; 182pp; English.
CC      The haemopoietin receptor (HR) NR6.2 is a form of the novel HR NR6.
CC      Interaction between the novel HR and a ligand facilitates proliferation,
CC      differentiation and survival of a wide variety of cells. The HR and its
CC      derivatives can be used for modulating the activity of the receptors e.g.
CC      to regulate development, maintenance or regeneration in an array of
CC      different cells and tissues in vitro and in vivo. They can be present in
CC      therapeutics used for modulating neuronal proliferation, differentiation
CC      and survival. The products can also be used for detection and diagnosis,
CC      e.g. for cancers or predisposition to cancers, or for drug screening.
SQ      Sequence 1673 BP; 344 A; 550 C; 474 G; 305 T;

Query Match          99.6%; Score 830.8; DB 1; Length 1673;
Best Local Similarity 99.8%; Pred. No. 3.2e-208;
Matches 832; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 cccaccccttctcagctcgcctccctcgaagctacgtcctctctatcatgagacacact 60
DB      275 cccaccccttctcagctcgcctccctcgaagctacgtcctctatcatgagacacact 334
QY      61 gggggcacgcgtgaggggctctactgagaccctcaatggtcgccgctgaccttgagctg 120
DB      335 gggggcacgcgtgaggggctctactgagaccctcaatggtcgccgctgaccttgagctg 394
QY      121 tcccgctccttcaacacctccacctggccctggccctggccctggccctggccctggccctg 180
DB      395 tcccgctccttcaacacctccacctggccctggccctggccctggccctggccctggccctg 454

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the haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and as tissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases, cancer, and allergy).

318 A;	552 C;	478 G;	308T:
Sequence	1656 Bp;		

181	QY	cs	gcagcagtcaggagacaatcttggtgtgtccacgcccgcagacgcgcagcattcttggttggtctcc	240
182	QY			
183	QY			
455	Db	CAGCAGTCAGGAGACAATCTGCTGTGTACGCCGCGAGACGSCAGCATCTGGCTGGCTCC	514	
456	Db			
241	QY	tcacctatgttgcttgcctcccttgagaagccctttaacatcagctgctggtccccgaac	300	
242	QY			
515	Db	TGCTCTATGTTGGCTTGCCCTGTGAGAAGCCCTTTACATCAGCTGCTGGTCCCGGAAC	574	
516	Db			
301	QY	atgaaggattctcacgtgcgctggacacccgggtgcacacggggagagacattcttacatacc	360	
302	QY			
575	Db	ATGAAGGATCTCACGTGCGCTGGACACCGGTGCACACGGGAGACATCTTACATAACC	634	
576	Db			
361	QY	aactactccctcaagtacaagctgaagtggttacggtcagagataacacatgtgaggagtac	420	
362	QY			
635	Db	AACTACTCCCTCAAGTACAAGCTGAGGTGGTACGGTCAGGATACACATGTGAGGAGTAC	694	
636	Db			
421	QY	cacactgtggggccccaactcatgccatatcccccaaggacctggccctcttcacacctat	480	
422	QY			
695	Db	CACACTGTGGGCCCTCACTCATGCCATATCCCAAGGACCTGGCCCTTTCACCTCCGCTAT	754	
696	Db			
481	QY	gagatctgggttggagccaccacaatcgcttagctcagcaagatctgatgtctcacaactg	540	
482	QY			
755	Db	GAGATGTGGGTGGAAAGCCACCACCAATCGCTAGGCTCAGCAAGATCTGATGCTCTCACACTG	814	
756	Db			
541	QY	gatgtcttgacgttggttaaccacgacacccccaccgccgctgcagtgagccgcgttggg	600	
542	QY			
815	Db	GATGTCTGGAGTGTGTGACACAGGACCCCCACCCTCCAGCTGCACGTGAGCCGCGTGTGG	874	
816	Db			
601	QY	ggcctggaggaaccagctgagtgctgcgctgggttctcaccaccagctctccaaggattctc	660	
602	QY			
875	Db	GGCCTGGAGGACCAGCTGAGTGTGGCTGGGTCTCACCACCAGCTCTCAAGGATTTCCTC	934	
876	Db			
661	QY	ttccaaagcaagtaccagatccgctaccgctggtggagagacagcgtggactggaaggttggtg	720	
662	QY			
935	Db	TTCCAAGCCAAGTACCAGATCCGCTACCGCTGSGAGSACACGCTGAGCTGGAAGGTGGTG	994	
936	Db			
721	QY	gatgcgctcagcaaacacagacctctgcgctctcgcgccctggaagcccgccagccggtttac	780	
722	QY			
995	Db	GATGAGCTCAGCAACCAGACCTCTCGCCGTCTCGCGGCCCTGAAGCCCGGACCGCTTAC	1054	
996	Db			
781	QY	ttcgtccaagtgcggttgaacccattcgggatctatggttgagaaaaagccggga	834	
782	QY			
1055	Db	TTCGTCCAAGTGGGTTGAACCATTCGGGATCTATGGGTCAAAAGCGGGA	1108	
1056	Db			

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RESULT      5
V41688
ID      V41688 standard; cDNA; 1656 BP.
AC      V41688;
DT      26-OCT-1998 (first entry)
DE      Nucleotide sequence of the murine U4 gene.
KW      Murine; U4 protein; haematopoietin receptor superfamily;
KW      cell proliferation; immune response; antibody; cell differentiation;
KW      autoimmune disease; cancer; allergy; ds.
OS      Mus sp.
FH      Location/Qualifiers
FT      122..1399
FT      /*tag= a
FT      /product= "U4 protein"
FT      W09831811-A1.
PN      23-JUL-1998.
PF      15-JAN-1998; U00334.
PR      16-JAN-1997; US-784863.
PA      (GEMMY) GENETICS INST INC.
PI      Collins M, Donaldson DD, Neben T, Whitters M;
PI      WPI; 98-414109/35.
DR      R-PSDB; W59804.
PT      New nucleic acid encoding U4 haematopoietin receptor superfamily
PT      chain - potentially useful, e.g. for modulating cell proliferation
PT      or immune response, for treating cancer and autoimmune disease
PS      Claim 1; Pages 25-26; 38pp; English.
CC      This is the nucleotide sequence encoding the murine U4 protein from

```

QY	361	aactactccctcaagtcacagctgaggtggtgtaagtcaggtacacatacacatgtgagaggtac	420
Db	669	AACTACTCCCTCAAGTCAACAGCTGAGTGGTGTATGTTGTCAGGACACACATGTGAGGAATAT	728
QY	421	cacactgtggggccccactcatgccatattcccaaggaacgtggccctcttcacitccctat	480
Db	729	CACACTGTGGGCCCTCACTCTGTCCTATATCCCAAGACCTGGCCCTCTTCACGCCCTAT	788
QY	481	gagatctgggtggaagcccaacatcgcctagctcagcaagatctgattgtctcacactg	540
Db	789	GAGATCTGGTGGGAAGCCACCAATCGCTGGGTTCAGCGAGATCTGACGTGCTCACACTG	848
QY	541	gattctctgagctggtgacacagggacccccaccacccagcgtgacgtgagcgcgttggg	600
Db	849	GATGTCCTGGACGTGTGTGACACAGGACCCTCCACCCGACGTGACGTGACGCCGCTTGGG	908
QY	601	ggcctggagaccagctgagctggtgctcaccacagctctcaagattctctc	660
Db	909	GGCCTGGAGGACCACTGAGTGTGCTGGCTGGGTCTCACCACAGCTCTCAAGGATTTCTC	968
QY	661	ttccaagccaagtaccagatccgctaccgcgtggaggacagcgtggactggaaggtgtgtg	720
Db	969	TTCCAAGCCAAATACCAGATTGCTACCGCGTGGAGACAGCGTGGACTGGAAGGTGGTG	1028
QY	721	gatacgtcagcaaccagacctctgcgtctcgcgtggccctgaagcccgacacgtttac	780
Db	1029	GATGACGTGACGACCAACGACACTCTCTGCCCTCTCGCGGGCTTGAAGCCGCGACCGTTTAC	1088
QY	781	ttcgtccaagtgtgtgttaaccattcgggatctatgggtcgaaaaagggcgggga	834
Db	1089	TTCTGTCCAAGTTCGTTGTAAACCAATTCGGGATCTATGGTCTGAAAAAGGGCGGA	1142
RESULT	7		
W70895			
ID	W70895	standard; cDNA; 1813 BP.	
AC	W70895		
DT	17-MAR-1999	(first entry)	
DE	CDNA encoding an allelic variant of human Zcytor5.		
KW	Zcytor5; cytokinin-like receptor; down-regulation; growth factor;		
KW	maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;		
KW	cardiac pathology; heart enlargement; Zcytor5 ligand; allelic variant;		
KW	SS.		
FS	HO	Homo sapiens.	
FT	Key	Location/Qualifiers	
FT	CDS	88..1365	
FT		/*tag-	
FT		a	
FT		/product= Zcytor5	
PN	W09849307-Al.		
PD	05-NOV-1998.		
PF	01-MAY-1998; U08865.		
PR	13-FEB-1998; US-074721.		
PR	01-MAY-1997; US-045287.		
PR	01-MAY-1997; US-850030.		
PR	13-FEB-1998; US-023890.		
PA	(ZIMO) ZYMOGENETICS INC.		
PI	Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,		
PI	Lok S, Presnell SR, Whitmore TE;		
DR	WFL; 99-034662/03.		
DR	P-PSDB; W70861.		
PT	New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.		
PT	down-regulating Zcytor5 natural ligands or detecting cardiotoxin-1		
PT	in blood		
PS	Disclosure; Page 68-70; 55pp; English.		
CC	The present sequence encodes an allelic variant of protein designated		
CC	Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be		
CC	administered to down-regulate the effects of a growth and/or maintain		
CC	factor in thyroid, heart, and skeletal muscle for example to lessen the		
CC	effect of cardiotoxin-1 on cardiac pathologies, so preventing heart		
CC	enlargement. Zcytor5 could be used to detect cardiotoxin-1 in the		
CC	blood, and to discover other possible Zcytor5 ligands. A probe		
CC	comprising Zcytor5 DNA or RNA can be used to determine the presence		
CC	and integrity of the Zcytor5 gene on chromosome 19, aortobodies and th		

QY 595 gtgggggctggagaccagctagtgctggtggtctcaccacacagctctcaaggat 654
 |||||
 Db 421 GTCGGGGCTGGAGGACCAGCTAGGCTGGCTGGGTGGCCACCGCCCTCAAGGAT 480
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 QY 655 ttctcttccaagccaagtaccagatccgtaccgcggtggagagcagcgctgagctggaag 714
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 Db 481 TTCCTTTTCAAGCAATACCAATCCGCTACCGAGTGGAGGACAGTGTGGAATGGAAG 540
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 QY 715 gtggtgagtcagtcagcaa 734
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 Db 541 GTGGTGGACGATGTGACAA 560

RESULT 12

V27148
 ID V27148 standard; DNA; 11832 BP.
 AC V27148;
 DT 29-SEP-1998 (first entry)
 DE Nucleotide sequence for murine NR6 containing additional 5N sequence.
 KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
 KW cell survival; therapeutic; neuronal proliferation; drug screening; ss;
 KW Mouse.
 OS Mus sp.
 PN W09811225-A2.
 PD 19-MAR-1998.
 PF 11-SEP-1997; G02479.
 PR 11-SEP-1996; AU-002246.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA (DZIE/) DZIEGLEWSKA H E.
 PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
 PI Zhang J;
 DR WPI: 98-260970/23.
 DR P-PSDB: W55016.
 PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PT e.g. neuronal cells
 PS Claim 9; Fig 3: 182pp; English.
 CC The NR6 protein is a novel Haemopoietin receptor (HR). Interaction
 CC between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and it's
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 11832 BP; 2447 A; 3367 C; 3298 G; 2720 T;

Query Match 30.5%; Score 254.4; DB 1; Length 11832;
 Best Local Similarity 99.6%; Pred. No. 2.3e-57;
 Matches 255; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ccacacctctcatcggtctccctccctgcaagctacctgctctctatcatgagacacacct 60
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 Db 6356 CCCACCCCTCTCATCGGCTCCCTCTGCAAGCTACCTGCTCTATACATGGAGACACCT 6415
 |||||
 QY 61 ggggcccacgcgtgaggggctctactggaccctccaatggtcgccgctgcccctctgagctg 120
 |||||
 Db 6416 GGGGCCACCGCTGAGGGGCTCTACTTGGACCTTCATGTTGGCGCGCTGCTGAGCTG 6475
 |||||
 QY 121 tcccgccctcttaacacacctccaccctggccctggccctggctaaaccttaattgggtccagg 180
 |||||
 Db 6476 TCCCGCCCTCTTAACACCTCCACCTCCACCTGGCCCTGGCCCTGGCTTAATGGTCCAGG 6535
 |||||
 QY 181 cagcagtcagagacaacttggtgtgtacgccccgagacgagcattcttggtgctcc 240
 |||||
 Db 6536 CAGCAGTCAGGAGACAATCTGGTGTGTGTACGCCCGGAGCGGAGCATTCGCTGGCTCC 6595
 |||||
 QY 241 tgcctctatgttgct 256
 |||||
 Db 6596 TGCCTCTATGTGGCT 6611

RESULT 14

V70897
 ID V70897 standard; cDNA; 259 BP.
 AC V70897;
 DT 17-MAR-1999 (first entry)

RESULT 13

V27145
 ID V27145 standard; DNA; 6663 BP.
 AC V27145;
 DT 02-OCT-1998 (first entry)
 DE Nucleotide sequence of Murine NR6.
 KW Haemopoietin receptor; cell proliferation; cell differentiation;
 KW cancer; cell survival; therapeutic; neuronal proliferation; drug;
 KW screening; ss; Mouse.
 OS Mus sp.
 FH Key
 FT CDS
 FT 1182..1744
 FT /tag- a
 FT /product- "Murine NR6"
 FT /note- "No start or stop codon given"
 PN W09811225-A2.
 PD 19-MAR-1998.
 PF 11-SEP-1997; G02479.
 PR 11-SEP-1996; AU-002246.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA (DZIE/) DZIEGLEWSKA H E.
 PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
 PI Zhang J;
 DR WPI: 98-260970/23.
 DR P-PSDB: W55016.
 PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PT e.g. neuronal cells
 PS Claim 8; Page 108-114; 182pp; English.
 CC The NR6 gene encodes a novel Haemopoietin receptor (HR). Interaction
 CC between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and it's
 CC products can be used for modulating the activity of the receptors e.g. to
 CC regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 6663 BP; 1462 A; 1852 C; 1715 G; 1634 T;

Query Match 30.5%; Score 254.4; DB 1; Length 6663;
 Best Local Similarity 99.6%; Pred. No. 2e-57;
 Matches 255; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ccacacctctcatcggtctccctccctgcaagctacctgctctctatcatgagacacacct 60
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 Db 1185 CCCACCCCTCTCATCGGCTCCCTCTGCAAGCTACCTGCTCTATACATGGAGACACCT 1244
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 QY 61 ggggcccacgcgtgaggggctctactggaccctccaatggtcgccgctgcccctctgagctg 120
 |||||
 Db 1245 GGGGCCACCGCTGAGGGGCTCTACTTGGACCTTCATGTTGGCGCGCTGCTGAGCTG 1304
 |||||
 QY 121 tcccgccctcttaacacacctccaccctggccctggccctggctaaaccttaattgggtccagg 180
 |||||
 Db 1305 TCCCGCCCTCTTAACACCTCCACCTCCACCTGGCCCTGGCCCTGGCTTAATGGTCCAGG 1364
 |||||
 QY 181 cagcagtcagagacaacttggtgtgtacgccccgagacgagcattcttggtgctcc 240
 |||||
 Db 1365 CAGCAGTCAGGAGACAATCTGGTGTGTGTACGCCCGGAGCGGAGCATTCGCTGGCTCC 1424
 |||||
 QY 241 tgcctctatgttgct 256
 |||||
 Db 1425 TGCCTCTATGTGGCT 1440

DE Expressed sequence tag used to identify human Zcytor5.
 KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; zcytor5 ligand; EST; ss.
 OS Unidentified.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI; 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
 PT down-regulating Zcytor5 natural ligands or detecting cardiostrophin-1
 PT in blood
 PS Example 1; Page 77; 55pp; English.
 CC The present sequence represents an expressed sequence tag (EST)
 CC used to identify cDNA encoding a protein designated Zcytor5, which is
 CC a cytokinin-like receptor. Soluble Zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytor5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible Zcytor5 ligands. A probe
 CC comprising Zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytor5 and
 CC therapeutically to modify Zcytor5 ligand effects.
 SQ Sequence 259 BP; 53 A; 64 C; 81 G; 46 T;

Query Match 15.4%; Score 128.8; DB 1; Length 259;
 Best Local Similarity 83.2%; Pred. No. 5.3e-25;
 Matches 153; Conservative 0; Mismatches 30; Indels 1; Gaps 1;
 QY 650 agatttcctctccaagcagatccgacgctacgcggtgagacagcgtggact 709
 Db 1 AGATTTCCTCTTTCAAGCCAATACACAGATCCGTGTCGATGAGGAGGAGTGGANT 60
 QY 710 gaaagtgtgtgatcagtcagcaaccagacacctcgtcgcgtcggtgagccg 769
 Db 61 GGAAGGTGTGGANGATGTGACCAACACACACCTTCTGCGG-CTGNCGCCCTGAAACCG 119
 QY 770 gacgctttactctcgaagtgcgttgaaccattcggtggtatctatgggtcgaaagg 829
 Db 120 GCACGTGTACTTCGTGCAAGTGCCTGCAANCCCTTTGGCATCTATGGCTNCAAGAAG 179
 QY 830 cggg 833
 Db 180 CCGG 183

RESULT 15

V70899
 ID V70899 standard; cDNA; 210 BP.
 AC V70899;
 DT 17-MAR-1999 (first entry)
 DE Expressed sequence tag used to identify human Zcytor5.
 KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; Zcytor5 ligand; EST; ss.
 OS Unidentified.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.

PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI; 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
 PT down-regulating Zcytor5 natural ligands or detecting cardiostrophin-1
 PT in blood
 PS Example 1; Page 77; 55pp; English.
 CC The present sequence represents an expressed sequence tag (EST)
 CC used to identify cDNA encoding a protein designated Zcytor5, which is
 CC a cytokinin-like receptor. Soluble Zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytor5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible Zcytor5 ligands. A probe
 CC comprising Zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytor5 and
 CC therapeutically to modify Zcytor5 ligand effects.
 SQ Sequence 210 BP; 31 A; 84 C; 57 G; 34 T;
 Query Match 9.7%; Score 81.2; DB 1; Length 210;
 Best Local Similarity 83.6%; Pred. No. 1.4e-12;
 Matches 92; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
 QY 1 cccaccctctctcgcgctcctccctcgaagctaccgtctctacatggagacacact 60
 Db 101 CCCAGCTTCTCATCGGCTCCTCCTGCTGCCACCTGCTCAGTCACGAGAGACCCACCA 160
 QY 61 gggggccaccgctgaggggctctactggaccctcaatgggtcgccgctgccc 110
 Db 161 GGAGCCACCGCGGAGGGCCTCTACTGGACCTCAACGGGCGCGGTGCC 210
 Search completed: September 28, 1999, 16:45:58
 Job time: 7343 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 28, 1999, 16:40:05 ; Search time 152.56 Seconds
(without alignments)
501.168 Million cell updates/sec

Title: US-09-037-657-18

Perfect score: 834

Sequence: 1 cccacccctctcgcgtc.....atgggtcgaaaaaggcgga 834

Scoring table: IDENTITY_NUC

Searched: 176461 seqs, 45838279 residues

Database: Issued_Patents_NA:**
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCRUS9_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	4.4	7218	2	US-08-232-463-14
2	35.4	4.2	423	2	US-08-470-179-109
3	34	4.1	15664	1	US-08-402-282-3
4	34	4.1	15664	1	US-08-508-004-3
5	34	4.1	15664	1	US-08-402-066-3
6	34	4.1	15664	1	US-08-402-068-3
7	33.4	4.0	1018	1	US-08-444-083-6
8	33.4	4.0	1018	1	US-08-286-304-6
9	33.4	4.0	1018	1	US-08-442-745-6
10	33.4	4.0	1018	1	US-08-443-129-6
11	33.4	4.0	1018	2	US-08-443-952-6
12	33.4	4.0	1018	2	US-08-443-130-6
13	33.4	4.0	1018	5	PCT-US95-04467-6
14	33.2	4.0	49272	3	US-08-614-770A-1
15	32.4	3.9	44377	4	US-08-804-227C-7
16	32.2	3.9	3234	2	US-08-264-534-31
17	32.2	3.9	3234	3	US-08-083-590A-10
18	32.2	3.9	3234	3	US-08-465-500-31
19	32.2	3.9	3234	4	US-08-346-128-31
20	32	3.8	3435	2	US-08-366-577-1
21	32	3.8	1055	4	US-08-828-242-2
22	32	3.8	3435	5	PCT-US96-00008-1
23	31.6	3.8	423	2	US-08-470-179-111
24	31	3.7	1897	4	US-08-532-547-6
25	31	3.7	1897	4	US-08-532-547-8
26	31	3.7	1715	5	PCT-US95-02315-1
27	30.6	3.7	3133	1	US-08-162-809-1
28	30.4	3.6	423	2	US-08-470-179-107
29	30.2	3.6	4884	1	US-07-665-792B-10
30	30.2	3.6	16885	2	US-08-390-878-16
31	30	3.6	1035	1	US-07-975-526-4
32	30	3.6	3293	1	US-07-923-976-1
33	29.8	3.6	1405	1	US-08-035-558-3
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35	29.8	3.6	1405	4	US-08-682-847-5
36	29.8	3.6	3468	4	US-08-459-448A-2
37	29.8	3.6	13987	4	US-08-804-227C-13

ALIGNMENTS

RESULT 1

```

: Sequence 14, Application US/08232463
: Patent No. 5670367
: GENERAL INFORMATION:
: APPLICANT: DORNER, F.
: APPLICANT: SCHEIFLINGER, F.
: APPLICANT: FALKNER, F. G.
: TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley & Lardner
: STREET: 1800 Diagonal Road, Suite 500
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22313-0299
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/232,463
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/935,313
: FILING DATE:
: APPLICATION NUMBER: EP 91 114 300.6
: FILING DATE: 26-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: BENT, Stephen A.
: REGISTRATION NUMBER: 29,768
: REFERENCE/DOCKET NUMBER: 30472/114 IMMU
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703)836-9300
: TELEFAX: (703)883-4109
: TELEX: 899149
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7218 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: CLONE: pTZgpt-Fls
: US-08-232-463-14

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Query Match 4.4%; Score 37; DB 2; Length 7218;
Best Local Similarity 1.3%; Pred. No. 0.49;
Matches 4; Conservative 176; Mismatches 121; Indels 0; Gaps 0;

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Db 1140 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1199
QY 61 gggggccacgcgtgagggggtctctactggaccctcaatggctgcgcgtgcctctctagctg 120

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Sequence 5, Appl1
Sequence 1, Appl1
Sequence 5, Appl1
Sequence 3, Appl1
Sequence 5, Appl1
Sequence 1, Appl1
Sequence 3, Appl1
Sequence 3, Appl1

Db 1200 YY 1259
QY 121 tccgcctccttaaacctccacccctgcccctggcctgtaacctaaatgggcccagg 180
Db 1260 YY 1319
QY 181 cagcagtcagagacaatctgtgtgtcaccgccgagacgagcagcattctgctggtccc 240
Db 1320 YY 1379
QY 241 tgcctctatgttgctcccccctcagagcccttaacatcagctgctggtcccggaac 300
Db 1380 YY 1439
QY 301 a 301
Db 1440 A 1440

RESULT 2

US-08-470-179-109
; Sequence 109, Application US/08470179
; Patent No. 5645994
; GENERAL INFORMATION:
; APPLICANT: Huang Ph.D, Wai Mun
; TITLE OF INVENTION: Method and Compositions for
; TITLE OF INVENTION: Identification of Species in a Sample
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Trask, Britt and Rossa
; STREET: P.O. Box 2530
; CITY: Salt Lake City
; STATE: Utah
; COUNTRY: USA
; ZIP: 84110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,179
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sweigert Ph.D, Susan E.
; REGISTRATION NUMBER: 36,289
; REFERENCE/DOCKET NUMBER: 2601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 801-532-1922
; TELEFAX: 801-531-9168
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Actinomyces naesundii
US-08-470-179-109

Query Match 4.28; Score 35.4; DB 2; Length 423;
Best Local Similarity 54.18; Pred. No. 0.58;
Matches 72; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 663 caagcccaagtaccagatccgctacgctgagagacgctgactggaagggtgga 722
Db 273 CTGGCCATGGAGATGCTCCGGGACATCGACGAGACAGCGTGCAGTCCAGGACAACTA 332

QY 723 tgacgtcagcaaccagacctctgcctgcctgcctgcctgcctgcctgcctgcctgcct 782
Db 333 CGAGCGGCAAGAACAGGAGCGGCTCATCTCGCGCGCGCGCTCCCGAACCTCTGGTCAA 392
QY 783 cgtcaagtgcgt 795
Db 393 CGGCTCGAGGGT 405

RESULT 3

US-08-402-282-3
; Sequence 3, Application US/08402282
; Patent No. 5476768
; GENERAL INFORMATION:
; APPLICANT: Pearson, Robert E.
; APPLICANT: Dickson, Julie A.
; APPLICANT: Hamilton, Paul T.
; APPLICANT: Little, Michael C.
; APPLICANT: Bever Jr., Wayne F.
; TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
; TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; COMPANY: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
; ZIP: 07417
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,282
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3283
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 222..425 /function= "potential open reading
; OTHER INFORMATION: /function= "frame"
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 451..747 /function= "potential open reading
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; NAME/KEY: misc.feature
; LOCATION: 747..1109 /function= "potential open reading
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; NAME/KEY: misc.feature
; LOCATION: 2034..2747


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Db 12338 ACCAGGACGACCGAGGACGAGCGCCGCTGCAGTCCCTCGCGGACGAGCAGCGCGCGG 12395

RESULT 5
US-08-402-066-3
; Sequence 3, Application US/08402066
; Patent No. 5612182
; GENERAL INFORMATION:
; APPLICANT: Pearson, Robert E.
; APPLICANT: Dickson, Julie A.
; APPLICANT: Hamilton, Paul T.
; APPLICANT: Little, Michael C.
; APPLICANT: Beyer Jr., Wayne F.
; TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
; TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
; ZIP: 07417
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,066
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3283
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15664 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; NAME/KEY: misc_feature
; LOCATION: 222..425
; OTHER INFORMATION: /function= "potential open reading
; OTHER INFORMATION: frame"
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; LOCATION: 451..747
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; LOCATION: 747..1109
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; OTHER INFORMATION: /function= "potential open reading
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; LOCATION: 12748..14499
; OTHER INFORMATION: /function= "potential open reading
; OTHER INFORMATION: frame"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 14771..15154
; OTHER INFORMATION: /function= "potential open reading
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; NAME/KEY: misc_feature
; LOCATION: 15154..15426
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; FEATURE:
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; LOCATION: 15429..15664
; OTHER INFORMATION: /function= "potential open reading
; OTHER INFORMATION: frame"
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US-08-402-066-3

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Query Match      4.1%; Score 34; DB 1; Length 15664;
Best Local Similarity 49.4%; Pred. No. 3.8;
Matches 88; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

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DB 12218 TCCGAAGACCGCCGGCGCTGTCGATGACCGGCCGGAACACGAGTACCGAGGCC 12277

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DB 12278 TGCTGGACCGCCCGGACGAGCGCATGAAGCGCAGAGGCCCGCGAGTTCACCGCCGCC 12337

QY 569 cccaccacgcagctgacgtgagccggttgggggcttgaggaccagctgagtgcg 626
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RESULT 6

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US-08-402-068-3
; Sequence 3, Application US/08402068
; Patent No. 5633159
; GENERAL INFORMATION:
; APPLICANT: Pearson, Robert E.
; APPLICANT: Dickson, Julie A.
; APPLICANT: Hamilton, Paul T.
; APPLICANT: Little, Michael C.
; APPLICANT: Bever Jr., Wayne F.
; TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
; TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
; ZIP: 07417
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,068
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3283
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15664 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 222..425
; OTHER INFORMATION: /function= "potential open reading
; OTHER INFORMATION: frame"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 451..747
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 747..1109
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; OTHER INFORMATION: frame"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1109..2014
; OTHER INFORMATION: /function= "potential open reading
; OTHER INFORMATION: frame"
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; LOCATION: 3109..3444
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; NAME/KEY: misc_feature
; LOCATION: 3444..3728
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; NAME/KEY: misc_feature
; LOCATION: 3731..4855
; OTHER INFORMATION: /function= "potential open reading
; OTHER INFORMATION: frame"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4855..5376
; OTHER INFORMATION: /function= "potential coding
; OTHER INFORMATION: sequence"
; OTHER INFORMATION: /product= "L5 gp37 homolog"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 5382..5747
; OTHER INFORMATION: /function= "potential open reading
; OTHER INFORMATION: frame"
; FEATURE:
; NAME/KEY: misc_feature

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Db 367 TTCAGTCGGCCTGGCGGACACACTGCGTCCAGACGCGGGGCGAGCGCGCCAGCGCC 308
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 Db 307 GCGCGTCCAGCGGACCGCTGCTGACTGGCAGCCCGCGTGGCTCGGAGCGGGGCG 248
 Qy 722 atagctcagcaaacagacacctcctgctgctcgcgggctgaagcccgccacccgtttact 781
 Db 247 CTCAGCGCGGCCACCGCGAGCGCGGGCGGAGAGCTGGGCGACCGCCGAGGGGTCTCCC 188
 Qy 782 tcg 784
 Db 187 TGG 185

RESULT 10
 US-08-443-129-6/C
 ; Sequence 6, Application US/08443129
 ; Patent No. 5627073
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Joffre
 ; APPLICANT: Chien, Kenneth
 ; APPLICANT: King, Kathleen
 ; APPLICANT: Pennica, Diane
 ; APPLICANT: Wood, William
 ; TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/443,129

FILING DATE: 17-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/233609

FILING DATE: 25-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 304

FILING DATE: (null)

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: 894P1D2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8674

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 1018 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-443-129-6

Query Match

Best Local Similarity 4.0%; Score 33.4; DB 1; Length 1018;

Matches 112; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

Qy 542 atgtctctggagctgtgtgacacaggaacccccacccgacgtgacagtgagcgggtgggg 601
 Db 427 AGGCCCCGGGCTTGGCGCGCGCGCTCTCCAGGCGGCGCAGCAGCGCGCGCGCGG 368
 Qy 602 gcttggagggaccagctagtgtgctggtgtctcaccaccagctctcaaggattctct 661
 Db 367 TTACAGTCGGCCGTGGCGGCGACACACTGCGTCCAGCAGCGGGGCGACGCGCGCC 308
 Qy 662 tccaagtcagtaaccagatccgctacccgctgagagacagcgtgagtggtggtg 721
 Db 307 GCGCGTCCAGCGGACCGCTGCTGACTGGCAGCCCGCGTGGCTCGGAGCGGGGCG 248
 Qy 722 atgacgtcagcaaacagacacctcctgctgctcgcgggctgaagcccgccacccgtttact 781
 Db 247 CTCAGCGCGGCCACCGCGAGCGCGGGCGGAGAGCTGGGCGACCGCCGAGGGGTCTCCC 188
 Qy 782 tcg 784
 Db 187 TGG 185

RESULT 11
 US-08-443-952-6/C
 ; Sequence 6, Application US/08443952
 ; Patent No. 5679545
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Joffre
 ; APPLICANT: Chien, Kenneth
 ; APPLICANT: King, Kathleen
 ; APPLICANT: Pennica, Diane
 ; APPLICANT: Wood, William
 ; TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/443,952

FILING DATE: 17-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/233609

FILING DATE: 25-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/286304

FILING DATE: 05-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: 894P1D4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8674

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 1018 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-443-952-6

Best Local Similarity 46.1%; Pred. No. 2.5;
Matches 112; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

QY 542 atgtctgtgagcgtggtgacacagcagcccccacccagcgtgcaagtgcagcgtgagcgcgttgggg 601
 Db 427 AGGCGCGGCGCCTGGCGCGCGCGGTCTCCAGGCGGCGCAGCAGCGCGCGCGCGG 368
 QY 602 gctgtggaggaccagctgagtgtgctgtgggttctcaaccacagctctcaaggatttctct 661
 Db 367 TTCAGCTCGCGCTGGCGCGCACACACTGCTCCAGCAGCGGGGCGCAGCGCGCGCGCC 308
 QY 662 tccaagccaagtaccagatccgtaccgcgtgagggacagcgtggactggaagtgtgtg 721
 Db 307 GCGCGCTCCAGCGCGCGCGCTGCTGACTGGCAGCGCGCGCGCTGGCTCGGAGCGCGCGG 248
 QY 722 atgactcagcaacacagacacctctgcgtctcgtggtcgtgagccctgaagcccgacacgttact 781
 Db 247 CTCAGGCG 188
 QY 782 tcy 784
 Db 187 TGG 185

RESULT 14

US-08-614-770A-1
 ; Sequence 1, Application US/08614770A
 ; Patent No. 5773267
 ; GENERAL INFORMATION:
 ; APPLICANT: WILLIAM R. JACOBS AND GRAHAM F. HATFULL
 ; TITLE OF INVENTION: D29 SHUTTLE PHASIDS AND USES THEREOF
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
 ; STREET: 90 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 10016

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE
 MEDIUM TYPE: DISKETTE
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/614,770A
 FILING DATE: MARCH 7, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: ELIZABETH A. BOGOSTAN
 REGISTRATION NUMBER: 39,911
 REFERENCE/DOCKET NUMBER: 96700/402
 TELEPHONE: (212) 286-0854 or 286-0082
 TELEX: TWX 710-581-4766
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 49272
 TYPE: NUCLEIC ACID
 STRANDEDNESS: DOUBLE
 TOPOLOGY: LINEAR

MOLECULE TYPE:
 DESCRIPTION: OLIGONUCLEOTIDE
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: MYCOBACTERIOPHAGE
 INDIVIDUAL ISOLATE: D29

Query Match 4.0%; Score 33.2; DB 3; Length 49272;

Best Local Similarity 59.6%; Pred. No. 8.4;
 Matches 56; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 690 cgtggaggacagcgtgactgggaagtggtggatgcagcaaccagacacctctctg 749
 Db 3800 CTTCCGCGGTGGCGGTACCTTCGACGGCGGTCAAGAACTTCTTCAACGGCTTCTCCGGCT 3859
 QY 750 tctcgggggctgaagccggaccgtttacttc 783
 Db 3860 GATCGCGCGGTGAACACCGTCAACGTCGACTTC 3893

RESULT 15

US-08-804-227C-7/c
 ; Sequence 7, Application US/08804227C
 ; Patent No. 5876991
 ; GENERAL INFORMATION:
 ; APPLICANT: DeHoff, Bradley S.
 ; APPLICANT: Kubstoss, Stuart A.
 ; APPLICANT: Rostock, Paul R., Jr.
 ; APPLICANT: Sutton, Kimberly L.
 ; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: THOMAS G. PLANT 1501
 ; STREET: LILLY CORPORATE CENTER
 ; CITY: INDIANAPOLIS
 ; STATE: IN
 ; COUNTRY: USA
 ; ZIP: 46285

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: ASCII(DOS) Text only
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/804,227C
 FILING DATE: February 21, 1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Plant, Thomas, G.
 REGISTRATION NUMBER: 35,784
 REFERENCE/DOCKET NUMBER: X-8231
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 317-276-2459
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4437 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 350..14002
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 NAME/KEY: CDS
 LOCATION: 14046..20036
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 20110..31284
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 NAME/KEY: CDS
 LOCATION: 31329..36071
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 LOCATION: 36155..41830

US-08-804-227C-7

Query Match 3.9%; Score 32.4; DB 4; Length 44377;

Best Local Similarity 47.9%; Pred. No. 13;
 Matches 93; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 28, 1999, 15:38:13 ; Search time 2095.87 Seconds
(without alignments)
784.921 Million cell updates/sec

Title: US-09-037-657-18

Perfect score: 834

Sequence: 1 cccaccccttcacggctc.....atgggtcgaaaaagcgggga 834

Scoring table: IDENTITY_NUC

Searched: 2546578 seqs, 986266752 residues

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- 50: gb_est31:*
- 51: gb_est32:*
- 52: em_est20:*
- 53: em_est21:*

- 54: em_est22:*
- 55: em_est23:*
- 56: em_est24:*
- 57: em_est25:*
- 58: em_est26:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	307.6	36.9	474	46	AI421423	AI421423 tf25h01.x
5	306	36.7	477	43	AI185924	AI185924 ge50c05.x
6	298.8	35.8	462	45	AI394468	AI394468 tf79d12.x
7	297.2	35.6	466	43	AI161002	AI161002 gb69g04.x
8	297.2	35.6	466	43	AI185780	AI185780 ge44h04.x
9	269	32.3	431	45	AI333812	AI333812 gp93e12.x
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11	245	29.4	417	44	AI269388	AI269388 q126b05.x
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19	115.2	13.8	235	48	AI575060	AI575060 UI-R-G0-u
20	90.8	10.9	237	25	N78873	N78873 zb17h05.s1
21	69	8.3	404	42	AI074921	AI074921 oy04d08.s
22	53	6.4	503	29	AA049278	AA049278 mj45c04.r
23	48.4	5.8	448	26	W46603	W46603 zc32h10.r1
24	43.4	5.2	457	26	W81301	W81301 zd85a12.r1
25	40.6	4.9	466	38	AA788346	AA788346 r7c10a1.r
26	39.4	4.7	438	30	AA255111	AA255111 mz79d08.r
27	39.4	4.7	391	41	AI049345	AI049345 uc83f01.y
28	39.4	4.7	377	43	AI226602	AI226602 uj10d11.y
29	39.4	4.7	466	43	AI226924	AI226924 uj10d11.y
30	38.4	4.7	562	44	AI315965	AI315965 uj28c06.y
31	38.4	4.7	529	49	AI663357	AI663357 uk27h09.y
32	38.4	4.6	575	49	AI663511	AI663511 uk33q04.y
33	38.4	4.5	458	27	AA043001	AA043001 zk56f01.r
34	37.4	4.5	379	39	AA884366	AA884366 al60c02.s
35	37.2	4.5	424	43	AI210597	AI210597 j9e06a1.r
36	36.2	4.3	404	48	AI555417	AI555417 UI-R-C2p-
37	36	4.3	365	34	AA509386	AA509386 vg18d09.r
38	35.6	4.3	362	43	AI211378	AI211378 o8g12a1.r
39	35	4.2	453	47	AI534183	AI534183 SD06722.5
40	35	4.2	622	49	AI637136	AI637136 603001A11
41	34.8	4.2	441	42	AI141310	AI141310 oy51b09.s
42	34.6	4.1	319	35	C26580	C26580 C26580 Rice
43	34.6	4.1	485	48	AI575103	AI575103 UI-R-G0-u
44	34.6	4.1	411	48	AI579792	AI579792 UI-R-AGO-
45	34.6	4.1	409	51	AI713798	AI713798 UI-R-AA1-

ALIGNMENTS

RESULT 1

AA049280

LOCUS

DEFINITION

clone IMAGE:479043 5' similar to SW-IL6B_MOUSE Q00560 INTERLEUKIN-6

RECEPTOR BETA CHAIN PRECURSOR ; mRNA sequence.

ACCESSION

AA049280

NID

AA049280

464 bp

mRNA

EST

30-DEC-1996

```

VERSION      AA049280.1  GI:1755311
KEYWORDS     EST.
SOURCE       house mouse.
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS      Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 464)
              Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
              Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
              Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
              Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
              Waterston, R.
TITLE        The WashU-HMI Mouse EST Project
JOURNAL      Unpublished (1996)
COMMENT      On Dec 30, 1996 this sequence version replaced gi:1528951.

Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 437.
MGI:289787
Location/Qualifiers
1. 464
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:479043"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTACCAACATCGAAGTGGAGCGCGCGGAATTTTTTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."
BASE COUNT   102 a 144 c 130 g 88 t
ORIGIN

Query Match      55.3%; Score 460.8; DB 29; Length 464;
Best Local Similarity 99.6%; Pred. No. 2.3e-107;
Matches 462; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 284 gctggtggtccggagacatgaagatctcagtcggtgacccgggtgcacacgggg 343
Db 1 gctggtggtccggagacatgaagatctcagtcggtgacccgggtgcacacgggg 60
Qy 344 agacattctacataccaaactactccctcaagtacacagctgaggtgtacggtcaggata 403
Db 61 AGACATCTTTACATACCAACTACTCCCTCAAGTACAGCTGAGTGTGCTACGGTCAGGATA 120
Qy 404 acacatgtgagagatcacacactgtggggcccccactatgcattcccaagacactgg 463
Db 121 ACACATGTGAGAGTACACACTGTGGGCCCTCTACTATGTCATATCCCCAAGGACCTGG 180
Qy 464 cccttctcactccctatgagatctgggtgggaagccacaaatcgctcaggtcagcaagat 523
|||||

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```

Db 181 CCCTCTTCACTCCCTATGAGATCTGGGTGGAAGCCACCACCAATCGCTAGGCTCAGCAAGAT 240
Qy 524 ctgatgtctcacactggtgctcctggagcgtggtgacacagcagccccccacccgacgtgc 583
|||||
Db 241 CTGATGTCTCACACTGATGTCTTGAGCTGTGTGACACGACGACCCGCCACCCGACGTGC 300
Qy 584 acgtgagcgcgttgggggcccctggaggaccagctgagtgctgctgggtgctcaccacag 643
|||||
Db 301 AGGTGAGCGCGCTTGGGGCCCTGGAGGACCACTGAGTGTGGCTGGGTCTCACCACCAG 360
Qy 644 ctctcaagattctctctccaagccaagtagtaccagatccgtaccgctgggagggacagcg 703
|||||
Db 361 CTCTCAAGATTTCCTCTTCCAAGCCCAAGTACCAGATCCGCTACCCGCTGGAGGACAGCG 420
Qy 704 tggactggaagtggtggtgacgtcagtcagcaaccagacacctctgc 747
|||||
Db 421 TGGACTGGAAGTGTGCTGATGACGTGACGACCAACACGACCTCTGTC 464

RESULT      2
LOCUS       W66776/c
DEFINITION mel7b11.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
clone IMAGE:387741 5' similar to PIR:B38252 B38252 granuloctye
colony-stimulating factor receptor precursor ; , mRNA sequence.
ACCESSION   W66776
NID         G1375694
VERSION     W66776.1  GI:1375694
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 482)
AUTHORS     Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
              Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
              Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
              Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
              Waterston, R.
TITLE       The WashU-HMI Mouse EST Project
JOURNAL     Unpublished (1996)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:785250.

Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:239573
Possible reversed clone: similarity on wrong strand
Seq primer: ETPrimer
High quality sequence stop: 359.
Location/Qualifiers
1. 482
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/map="10 pter-gen"
/clone="IMAGE:387741"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
/cissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCGGAATTTTTTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."

```

14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2.]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo.

BASE COUNT 96 a 138 c 147 g 101 t
ORIGIN

Query Match 51.3%; Score 428.2; DB 26; Length 482;
Best Local Similarity 99.1%; Pred. No. 4.4e-99;
Matches 441; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 391 tacgtcaggataacacatgtgagaggtaccacactgtggggcccccactatgcataac 450
|||||
Db 482 TACGGTCAGGATAACACATGTGAGAGGTACCACACTGTGGGCCCTCACTATGCCATATC 423
|||||
QY 451 ccaaggacctggccctcttcactccctatagatctgtgggtggaagccaccaatgccta 510
|||||
Db 422 CCCAAGGACCTGGCCCTCTTCACTCCCTATGAGATCTGGTGAAGCCACCACCAATCGCCTA 363
|||||
QY 511 ggctcagcaagatctgtctccacactgattctctgagctgaggtggtgacacagacccc 570
|||||
Db 362 GGCTCAGCAGATCTGATGCTCTCACACTGATGTCCTGGACGTGGTGAACACGAGACCCC 303
|||||
QY 571 ccacccagctgcagctgagcgcgttggggcctggagaccagctgagtggtgcgtcg 630
|||||
Db 302 CCACCCGACGTGCAGGTGAGCGCGGCTGGGGCCCTGGAGGACCACTGAGTGTGGCTGG 243
|||||
QY 531 gtctcaccacagctctcaaggattctctcttctccaaagccaagtaccag-atccgctaccg 689
|||||
Db 242 GTCTCACCACAGCTCTCAAGGATTCTCTTCCAAAGCCAAGTACCAGTATTCCTACCG 183
|||||
QY 690 cgtggagacagctgactggaaggtgggtgagatgagctcagcagacacagacctctgcg 749
|||||
Db 182 CGTGGAGGACAGCTGACTGGAAGGTGGTGGATGACGTACAGCAACCAAGACCTCTGCGG 123
|||||
QY 750 tctcggggcctgaagcccgccacgcttactctgccaagtgtgttaaccattcgg 809
|||||
Db 122 TCTCGCGGGCTGAGCGCCGCGCACCGTTTACTTCCTCAAGTGTGTTATACCCATTCGG 63
|||||
QY 810 gatctatgggtcgaaagagcg99ga 834
|||||
Db 62 GATCTATGGTTCGAAAGGCGGGA 38
|||||

RESULT 3

AA866388 428 bp mRNA EST 05-FEB-1999
LOCUS
DEFINITION
UI-R-A0-aj-f-04-0-UI-s3 UI-R-A0 Rattus norvegicus cDNA clone
UI-R-A0-aj-f-04-0-UI-3' similar to gBAC003112|AC003112 Human DNA
from chromosome 19 specific cosmid R30292, genomic sequence,
complete sequence (Homo sapiens), mRNA sequence.

ACCESSION
NID AA866388
VERSION 94230568
KEYWORDS
SOURCE EST
ORGANISM Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 428)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
AUTHORS
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT On Mar 16, 1998 this sequence version replaced gi:2961849.

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping

University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: mscoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics
Seq primer: M13 Forward.

FEATURES

source
Location/Qualifiers
1. 428
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/map="between D1S1765 and UGB"
/clone="UI-R-A0-aj-f-04-0-UI"
/clone_lib="UI-R-A0"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; This library
consists of a mixture of individually tagged normalized
libraries constructed from rat placenta, adult lung,
brain, liver, kidney, heart, spleen, ovary, and muscle.
The tag is a string of 3-5 nucleotides present between the
Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture."

BASE COUNT 87 a 134 c 120 g 87 t
ORIGIN

Query Match 46.5%; Score 388.6; DB 45; Length 428;
Best Local Similarity 94.4%; Pred. No. 4.7e-89;
Matches 403; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 386 ggtgggtcagctcaggataacacatgtgaggtaccacactgtggggcccccactatgcc 445
|||||
Db 2 GGCGCTCAATCAGGACACACATGTGAGGAATATCACACTGTGGGCCCTCACTCGTGC 61
|||||
QY 446 atatcccccaggacctggccctcttcaactcctatgagatctggtgggaagccaccaatc 505
|||||
Db 62 ATATCCCAAGACCTGGCCCTCTTACGCGCCCTATGAGATCTGGTGAAGCCACCACCATC 121
|||||
QY 506 gcttaggtcagcaagatctgattctcctcacactggtatgctcctggagcgtgtgaccacgg 565
|||||
Db 122 GCCTGGTTTCAGCGAGATCTGACGTGCTCACACTGGATGTCTTGGACGTGGTGCACCGG 181
|||||
QY 566 acccccacccagctgcagctgagcgcgttggggcctggggaccagctgagtgctc 625
|||||
Db 182 ACCCTCCACCCGACGTGCACGTGAGCGCGCTTGGGGCCCTGGAGGACCACTGAGTGTGC 241
|||||
QY 626 gctgggtcttcaccacagctcctcaagattctcttcccaagcgaagtaccagatccgct 685
|||||
Db 242 GCTGGGTCTCACCAACCACTCTCAAGGATTTCTCTTCCAAAGCCAAATACCAATTGCGT 301
|||||
QY 686 accgcgtgggagacagctggtgactggaaggtgtggtgacgtcagcagcaaccacacctcct 745
|||||
Db 302 ACCGCGTGGAGGACAGCGTGGAGGTGTGGATGACGTACAGTACAGCAACCACTCCT 361
|||||
QY 746 gccgtctcggggcctgaagcccgccagcgtttactctgctccaaagtgcgttgtaaccatc 805
|||||
Db 362 GCCTCTTCGGGGCTTGAGGCCCGGACCGCTTTACTTCTGCTCAAGTTCGTTGTAACCCAT 421
|||||
QY 806 tcgggat 812
|||||
Db 422 TCGGGAT 428
|||||

RESULT 4

AA1421423
LOCUS
AI421423 474 bp mRNA EST 30-MAR-1999

DEFINITION tf25h01.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2097265 3' similar to SW:IL6B_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR ;, mRNA sequence.

ACCESSION AI421423

NID 94267354

VERSION AI421423.1 GI:4267354

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 474)

TITLE NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGA), Tumor Gene Index

COMMENT Unpublished (1998)

On Apr 7, 1998 this sequence version replaced gi:3034955.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 1664 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 450.

FEATURES

Location/Qualifiers

1..474

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone.lib="NCI_CGAP_Brn23"

/tissue_type="glioblastoma (pooled)"

/lab_host="DH10B"

/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCATATCTTTTITTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 81 a 181 c 128 g 83 t 1 others

Query Match 36.9%; Score 307.6; DB 46; Length 474;

Best Local Similarity 86.1%; Pred. No. 1.8e-68;

Matches 340; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 1 cccacccttcacggctctccctcgaagctacactctctctatatacattgggaccacct 60

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 80 CCCAGCTCTCATCGGCTCTCCCTGCTGCGCCACCTGCTAGTGCAGGAGACCCACCA 139

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 gggggccacggctgagggctctactgacacctcaatgtcccgctccctctgagctg 120

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 140 GGAGCCACCGCGGAGGGGCTCTACTTGGACCTCTCAATGGCGCGCTGCCCCCTGAGCTC 199

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 tcccgcctcttaacacacctccacctggccctggcctggcctaaacttaattgggtccagg 180

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 200 TCCCGTGACTACAGCGCTCCACCTTGCTGCTGGCCCTGGCCACACTCAATGGGTCCAGG 259

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 cagcagtcaggagacaatctggtgtgtcagcccgagcggcagcattctgctggtctcc 240

Db 260 CAGCGGTGGGGACACACCTCGTGTGCCACGCCCGTGCACGCACATCCTGGTGGCTCC 319

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 241 tgctctatgttgcttgcctccctcctgagaagccctttaacatcagctgctggtcccggaac 300

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 320 TGGCTCTATGTTGGCTGCGCCGCCAGAGAACCCGCTCAACATCAGCTGCTGCTCAAGAAC 379

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 301 atgaagatctcacgtgcctgcctggacacccgggtgcacacggggagacattcttaccatcc 360

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 380 ATGAAGACCTTGACCTGCCGCTGGACGCCAGGGGCCACCGNGAGACCTTCTCTCCACACC 439

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 361 aactactccctcaagtataaagctgaggtggtacgg 395

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 440 AACTACTCCCTCAAGTACAAGCTTAGTGCTATGG 474

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5

AI185924

LOCUS

DEFINITION

qe50c05.x1 Soares_fetal_lung_NDHL19W Homo sapiens cDNA clone

IMAGE:1742408 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR ;,

mRNA sequence.

ACCESSION

AI185924

NID

93736562

VERSION

AI185924.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 477)

AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

JOURNAL

On Feb 17, 1998 this sequence version replaced gi:2150926.

COMMENT

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1552 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 467.

FEATURES

Location/Qualifiers

1..477

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone.lib="Soares_fetal_lung_NDHL19W"

/dev_stage="19 weeks"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: lung; Vector: pT73D (Pharmacia) with a

modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer

[5'-TGTTACCAATCTGAAGTGGAGCGCGCATATCTTTTITTTTTTTT-3'];

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT73 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo. This library was constructed

from the same fetus as the fetal heart library, Soares

fetal heart NDHL19W."

BASE COUNT 81 a 183 c 129 g 83 t 1 others

ORIGIN

Query Match 36.7%; Score 306; DB 43; Length 477;

Best Local Similarity 85.8%; Pred. No. 4.5e-68;

Matches 339; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

```

/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTACCACTCACTGAAGTGGAGCGCGGCATATCTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
79 a 181 C 122 g. 79 t 1 others

```

7
RESULT
AII61002
LOCUS
AII61002
DEFINITION
IMAGE:1705398_3', mRNA sequence.
ACCESSION
AII61002
NID
Q3694307
VERSION
AII61002.1
KEYWORDS
GI:3694307
SOURCE
EST.
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 466)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor gene index
(Unpublished 1997)
On Jan 19, 1998 this sequence version replaced gi:2287379.
JOURNAL
COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.


```

RESULT 9
AI333812 431 bp mRNA EST 13-FEB-1999
LOCUS qp99ei2.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
DEFINITION IMAGE:1930606 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR ;,
mRNA sequence.
ACCESSION AI333812
NID 94070371
VERSION AI333812.1 GI:4070371
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 431)
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 14, 1998 this sequence version replaced gi:1797892.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1615 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 407.
Location/Qualifiers
1..431
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="4p16.1-4pter"
/clone="IMAGE:1930606"
/clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: lung; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TCTTACCAATCTGAAGTGGAGCGCGCGCAATTTTCTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NbHL19W."
BASE COUNT 68 a 169 c 122 g 72 t
ORIGIN
Query Match 32.3%; Score 269; DB 45; Length 431;
Best Local Similarity 85.7%; Pred. No. 1.1e-58;
Matches 299; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 cccacccttctatcgctcctcctcaagctaccctctctatcatgagacacacct 60
|||||
DB 83 CCCACGGTCTTCATCGGCTCTCCTCGTCCACCTGCTCAGTGCACGGAGACCCACCA 142
|||||

QY 61 gggggccaccgctgaggggcttactggaccctcaatggctggcgcctgctctgagctg 120
|||||
DB 143 GGAGCCACCGCGAGGGCCCTTACTGTGACCTCAACGGGCGCGCGCTGCCCTTGAGCTC 202
|||||

QY 121 tccgcctctctaaacacctccacctggcctggcctggctggttaaccttaattggtccagg 180
|||||
DB 203 TCCGCTACTCAACGCTCCACCTTGGCTGTGGCTGGCCCTGACCAACCTCAATGGGTCCAGG 262
|||||

QY 181 cagcagctcaggagacacatctggtgtgcaagcccgagacgagcagcattctgctggtcc 240
|||||

```

```

Db 263 CAGGGTCGGGGGACAAACCTCGTGTGCGACGCCGCTGACGGCAGCATCTCGTGCTGCTCC 322
QY 241 tgctctatgttggctggcccttgagaagcccttttaacatacagctgctggtcccggaac 300
|||||
Db 323 TGCTTATGTTGGCTGCGCCCGCAGAGAAACCGCTCAACATCAGCTGCTGTGTCACGAAC 382
|||||
QY 301 atgaagatctcagtcgctgacacgggtgacacgggtgacacgggtgacacgggtgacac 349
|||||
Db 383 ATGAGGACTTGACCTGCGCTGCGACGCCAGGGGCGCCACGGGGAGACCT 431
|||||

RESULT 10
AI187074 447 bp mRNA EST 29-OCT-1998
LOCUS qc38a03.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
DEFINITION IMAGE:1741228 3' mRNA sequence.
ACCESSION AI187074
NID 93737712
VERSION AI187074.1 GI:3737712
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 447)
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Aug 21, 1998 this sequence version replaced.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1667 Std Error: 0.00
Seq primer: -40ml3 fwd. Et from Amersham
High quality sequence stop: 431.
Location/Qualifiers
1..447
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1741228"
/clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: lung; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTATACCAATCTGAAGTGGAGCGCGCGCAATTTTCTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NbHL19W."
BASE COUNT 69 a 175 c 128 g 74 t 1 others
ORIGIN
Query Match 32.1%; Score 267.6; DB 43; Length 447;
Best Local Similarity 85.6%; Pred. No. 2.4e-58;
Matches 297; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 cccacccttctatcgctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 60
|||||
Db 101 CCCACGGTCTTCATCGGCTCTCCTCGTCCACCTGCTCAGTGCACGGAGACCCACCA 160
|||||

QY 61 gggggccaccgctgaggggcttactggaccctcaatggctggcgcctgctctgagctg 120
|||||

```



```

/db_xref="GDB:3760555"
/db_xref="taxon:9606"
/map="12p"

```

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa
Tel: 319 335 8350

Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA library Preparation: M.B.

Soares Lab Clone distribution: clones will be available through

Research Genetics (www.resgen.com)

Seq primer: M13 Forward.

Location/Qualifiers

```
1. 332
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-GO-ut-h-08-0-UI"
/clone_lib="UI-R-GO"
/dev_stage="adult"
/lab_host="PH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-GO
library is a normalized library constructed from a
mixture of rat tissues (nodose ganglia, dorsal root
ganglia, and trigeminal ganglia). The tag is a string of
6 nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996."
```

BASE COUNT 49 a 121 c 93 g 69 t

Query Match 23.8%; Score 198.4; DB 48; Length 332;

Best Local Similarity 92.9%; Pred. NO. 7.9e-41;

Matches 208; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
QY 1 ccacaccttctatcggtctccctcgacgtacctgtctctatcatgagacacacct 60
|||||
DB 109 CCACACTTCTCATCGGATCTCCCTCATGCTACGCTGCTATATACATGAGACACCG 168
|||||
QY 61 ggggcccaccgtgaggggtctactgacctcaatggtcgccgctgacctctgagctg 120
|||||
DB 169 GGGGCCACTGCTGAGGGCCCTCTACTGGACCCCTCAACGGCCGCCGCTCGCCCTCAGAGCTG 228
|||||
QY 121 tcccgctctctaaacctccacctggccctggccctgaccttaatgggtccagg 180
|||||
DB 229 TCCCGTCTCTCAACACTCCACCTCGCCTGGCTTGCCCTGGCTTAACCTTAATGGTCCAGG 288
|||||
QY 181 cagcagtcaggagacacatctggtgtgtcagcccgagacggcag 224
|||||
DB 289 CAGCAGTCAGGGGACAAATCTGGTGTGTACGCCCGAGATGGCAG 332
|||||
```

RESULT 15

AI574687

LOCUS

AI574687 319 bp mRNA EST 30-MAR-1999

UI-R-GO-uc-b-11-0-UI.s1 UI-R-GO Rattus norvegicus cDNA clone

UI-R-GO-uc-b-11-0-UI 3', mRNA sequence.

ACCESSION AI574687

NID 9454683

VERSION AI574687.1 GI:4544683

KEYWORDS EST.

SOURCE Norway rat.

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 319)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

JOURNAL 9704477

MEDLINE

COMMENT

On May 18, 1998 this sequence version replaced gi:3138307.

Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa

451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA library Preparation: M.B.

Soares Lab Clone distribution: clones will be available through

Research Genetics (www.resgen.com)

Seq primer: M13 Forward.

Location/Qualifiers

```
1. 319
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/map="6p21.3: 5q33"
/clone="UI-R-GO-uc-b-11-0-UI"
/clone_lib="UI-R-GO"
/dev_stage="adult"
/lab_host="PH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-GO
library is a normalized library constructed from a
mixture of rat tissues (nodose ganglia, dorsal root
ganglia, and trigeminal ganglia). The tag is a string of
6 nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996."
```

BASE COUNT 46 a 116 c 88 g 68 t 1 others

Query Match 22.3%; Score 186; DB 48; Length 319;

Best Local Similarity 92.4%; Pred. No. 1.1e-37;

Matches 195; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
QY 1 ccacaccttctatcggtctccctcgacgtacctgtctctatcatgagacacacct 60
|||||
DB 109 CCACACTTCTCTATCGGATCTCCCTCATGCTACGCTGCTATATACATGAGACACCG 168
|||||
QY 61 ggggcccaccgtgaggggtctactgacctcaatggtcgccgctgacctctgagctg 120
|||||
DB 169 GGGGCCACTGCTGAGGGCCCTCTACTGGACCCCTCAACGGCCGCCGCTCGCCCTCAGAGCTG 228
|||||
QY 121 tcccgctctctaaacctccacctggccctggccctgaccttaatgggtccagg 180
|||||
DB 229 TCNCGTCTCTCAACACTCCACCTCGCCTGGCCTTGCCCTGGCTTAACCTTAATGGTCCAGG 288
|||||
QY 181 cagcagtcaggagacacatctggtgtgtcagc 211
|||||
DB 289 CAGCAGTCAGGGGACAAATCTGGTGTGTCTCAGC 319
|||||
```

Search completed: September 28, 1999, 15:38:17

Job time: 3285 sec

prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the Frameplot program of Bibb et al., Gene 30:157-66(1984) as implemented at <http://www.nih.gov/jp/jun/cgi-bin/frameplot.pl>. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 9810 lies between 2E9 and 5B8 in the Aser-B genomic restriction fragment.

FEATURES

source

1. 33320
/organism="Streptomyces coelicolor"
/strain="A3(2)"

/db_xref="taxon:1902"

/clone="cosmid 9810"

complement(1..6675)

/note="overlap with Cosmid St5B8"

complement(159..905)

/gene="SC9B10.01c"

complement(159..905)

/gene="SC9B10.01c"

/note="SC9B10.01c, unknown, len: 248 aa"

/codon_start=1

/transl_table=11

/product="hypothetical protein SC9B10.01c"

/protein_id="CAA15791.1"

/db_xref="PID:el202332"

/db_xref="PID:g2661687"

/db_xref="GI:2661687"

/db_xref="SPTREMBL:O50508"

/translation="MRGADVFGAGCDPRFPCCASSPPRRSAPLGTLEAAPSFIAR
RSPADPHSTTGGSPGVDMVTKNATGRFGSAAGMLATAGISLAARRRREA
RMHRLLELEAIRQSLAQHQRHMLLRAIDPLSLAEVIDYDKSIPARRRQF
FYANAYVNLVHVRAGLLDQGLQRLEFFQSPVREYWEATNRRAALDQNSDEA
RLGLVDALAKFEDTDTDEWVVGTPPHD"

983..989

/note="possible RBS upstream of SC9B10.02"

997..2085

/gene="SC9B10.02"

997..2085

/gene="SC9B10.02"

/note="SC9B10.02, unknown ATP/GTP binding protein, len:

362 aa; similar in N-terminus to other ATP/GTP binding

proteins eg. COBW_PSEDE P29937 cow protein from

pseudomonas denitrificans (353 aa), fasta scores: opt: 302

z-score: 390.2 E(): 1.4e-14, 30.1% identity in 366 aa

overlap. Contains PS00017 ATP/GTP-binding site motif A

(P-loop).
/codon_start=1

/transl_table=11

/product="hypothetical protein SC9B10.02"

/protein_id="CAA15792.1"

/db_xref="PID:el202333"

/db_xref="PID:g2661688"

/db_xref="GI:2661688"

/db_xref="SPTREMBL:O50509"

/translation="MGQRSTPQPIPVVVVLAGFLSGKTTLLNHLHRSRGRICAVVN
DFGSEIDAMVAGLSDTVSLGNGCLCAVDASDELGLARLARAEADIVIVIA
SGLAEPOLYMLLASQPGIVGGLVEVDAAEFDDTRAHPEIDRHLLADLVVYN
KTRATDAERVGLVHSLVGAAVVPATYRIDPEFLYDCRPGEEVGOISLFDLHDH
SEGGAHADHLLHAAYDITLSFVSGPLDPRRLMRFLDSRPKGLYRIKGYVDFPYDTRN
YAVHVGVRFLRFYPTPEPTPAGAGGAPETGRTQLVIGSIDAAALGEELDACRED
ADAPPADHEGHWGLRVYVADGEPPDSP"

1045..1068

/gene="SC9B10.02"

/note="PS00017 ATP/GTP-binding site motif A (P-loop)"

misc_feature

gene

CDS

complement(2082..4538)

/gene="SC9B10.03c"

complement(2082..4538)

/gene="SC9B10.03c"

/note="SC9B10.03c, DNA gyrase-like protein, subunit A,
len: 818 aa; similarity (strongest in N-terminus, around
active site) to DNA gyrase subunit A from many organisms
eg. GYRA_MCTU Q07702 dna gyrase subunit a (ec 5.99.1.3)
from Mycobacterium tuberculosis (838 aa), fasta scores:
opt: 1835 z-score: 1379.9 E(): 0, 42.4% identity in 768 aa
overlap; and to S. coelicolor GYRA_STRCO P35885 dna gyrase
subunit a (ec 5.99.1.3) (864 aa), fasta scores: opt: 1886
z-score: 1425.4 E(): 0, 42.9% identity in 788 aa overlap.
Contains probable coiled-coil region from aa 441 to 486."

/codon_start=1

/transl_table=11

/product="DNA gyrase-like protein"

/protein_id="CAA15793.1"

/db_xref="PID:el202334"

/db_xref="PID:g2661689"

/db_xref="GI:2661689"

/db_xref="SPTREMBL:O50510"

/translation="MAARRSTKTPPPDDSYEERILDIVDEMGSFLEYAYSVIYSRA
LPDARDGLKPVHRRIVTQMNMGRPERGVKCARVVGVMGLKHPHGDAISVDALVR
MAQSFMRVPLVDGHNGFSIGNDPPAAMRYTECRNAEAGLMTESIDEDTVDFAFN
YDGOEPFVALPAAPFNLLVNGASGIVAGNATNPPHNREVIAAARHLRVLNADDD
ALMKHVPGDPLPTGGRIVGLPGINDAYETGRGTFKIRATSVETVARRRGLVVTLP
LVAMEPKVISKDLVAGKIQIADYKDLTDRAHGLRLVIEIKNGFVPAVLEQLYK
FATGESEFGNNVALVDGQPLTGLKELLEVLDRFTVVRSEFRSRKRRRLHLV
EGLLTALVDIDEVIRLSSENSAOKRIMERFSLSDVOTQILDTPLRLTKYDRI
ELESEKRLNAEIEELTRILDSAELEKLYSAELAARVAKKFGTDRRTLLSSGAPVA
AVPLQVADPCRVLLSSTGLLATANDEPLVTAGARVADHLVSAVPATARGEVG
VTSGRLRLRVNVDLPOLPEAMPPTNLAGGAPAEFVSLEDDVDCLTLDSSPGL
ALGTGQGVVRVVDYPSNKEDEVLTKDGRIVGVELTGDGDLVFTDDAQLLR
YQASQVRPQGRAGVAGVADKAGKISFTAVDPAADVFTVAGSRGTLDDSVQTT
AKLTPFGYPRKGRATGVCRCFLKGEDCLAFWAGATPALAAQNKGTAQLPDDPD
RRDGSGLSKPTVSVVAGPV"

complement(3040..4460)

/gene="SC9B10.03c"

/note="69% match EM_BA_SCDNAGYR L27063 Streptomyces

coelicolor dnaA-gyrA region from 5495 to 6921"

complement(4548..4553)

/note="possible RBS upstream of SC9B10.03c"

4865..4871

/note="possible RBS upstream of SC9B10.04"

4874..6226

/gene="SC9B10.04"

4874..6226

/gene="SC9B10.04"

/note="SC9B10.04, probable zinc protease, len: 450 aa;

weakly similar to many of prokaryotic and eukaryotic

origin eg. Y4WA_RHISN P55679 hypothetical zinc protease

Y4wa from Rhizobium sp. (512 aa), fasta scores: opt: 617

z-score: 325.0 E(): 6.1e-11, 30.8% identity in 426 aa

overlap; and MPP2_YEAST P10507 mitochondrial processing

peptidase beta subunit (462 aa), fasta scores: opt: 355

z-score: 321.6 E(): 9.4e-11, 25.3% identity in 415 aa

overlap. The zinc-binding and active site residues are

conserved"

/codon_start=1

/transl_table=11

/product="zinc protease"

/protein_id="CAA15794.1"

/db_xref="PID:el202335"

/db_xref="PID:g2661690"

/db_xref="GI:2661690"

/db_xref="SPTREMBL:O50511"

/translation="MPMGHTAQAGSGGLTATEHRLANGLRVLSDEHLTPAAVCL
WVDGSRHVRKGTGLAHLFEHLMFGSAQVKGNGHFLVQAGGSLNGCTSFERTNY
FETMPAHOELALWLEADRMGSLAALDDSENQDRVVKVNRORRYDNPVGTAFEK
LTALAYPEGHVHTPIGSMADLDAETLADAFRTYAPNNVLSVVGIDDPQTL
AMLEKYGSIASHDKGPKDPCALPDVGGELREVVEEVPARALMAAYRLPDEGTRA
CDAADLALVVGSGESSRLYNRLVRDRTAVAAAGFGLRLLAGAPSLGWLVDKTSGDVE


```

clone 365523 5' (428..496); 97% identity.--(13756..13984)
DSS similarity to AA009693 zeb2h02.s1 Soares fetal heart
NBH19W Homo sapiens cDNA clone 365523 3' (227..1); 98%
identity.--(13756..13984) DSS similarity to AA450010
zx33f04.s1 Soares total fetus NB2HF8 9w Homo sapiens cDNA
clone 788287 3' (228..1); 99% identity.--
complement(14100..14672)
/rpt_family="Alu"
14855..15317
/notes="DSS similarity to AA406406 zvile07.s1 Soares NBHMPU
s1 Homo sapiens cDNA clone 753348 3' (1..433); Score: 858
Identity: 431/433 (99%)--(14884..15237) DSS similarity
to W37175 zb21a02.r1 Soares fetal lung NBHL19W Homo
sapiens cDNA clone 302666 5' (1..355); 94%
identity.--(15227..14885) DSS similarity to AAL121532
zk89c11.s1 Soares pregnant uterus NBHPU Homo sapiens cDNA
clone 490004 3' (342..1); 99% identity.--(15227..14885)
DSS similarity to AAL127694 zk89c11.r1 Soares pregnant
uterus NBHPU Homo sapiens cDNA clone 490004 5' (126..467);
99% identity.--(15227..14897) DSS similarity to W46603
zc32h10.r1 Soares senescent fibroblasts NBHSF Homo sapiens
cDNA clone 324067 5' (328..1); 98%
identity.--(15227..15088) DSS similarity to W46604
zc32h10.s1 Soares senescent fibroblasts NBHSF Homo sapiens
cDNA clone 324067 3' (322..465); 96% identity."
15713..15760
/notes="DSS similarity to AAL121532 zk89c11.s1 Soares
pregnant uterus NBHPU Homo sapiens cDNA clone 490004 3'
(389..343); 99% identity.--DSS similarity to AAL127694
zk89c11.r1 Soares pregnant uterus NBHPU Homo sapiens cDNA
clone 490004 5' (77..125); 90% identity.--(15735..15713)
DSS similarity to W46603 zc32h10.r1 Soares senescent
fibroblasts NBHSF Homo sapiens cDNA clone 324067 5'
(351..329); 100% identity.--(15735..15713) DSS similarity
to W46604 zc32h10.s1 Soares senescent fibroblasts NBHSF
Homo sapiens cDNA clone 324067 3' (299..321); 100%
identity."
complement(15895..16082)
/notes="predicted exon, program: grill2exons_human_1.3,
frame: 0, quality: excellent, score: 81.000--other
overlapping matches:--(15936..15895) DSS similarity to
AAL121532 zk89c11.s1 Soares pregnant uterus NBHPU Homo
sapiens cDNA clone 490004 3' (431..390); 100%
identity.--(15970..15895) DSS similarity to AAL127694
zk89c11.r1 Soares pregnant uterus NBHPU Homo sapiens cDNA
clone 490004 5' (1..76); 100% identity."
17926..18190
/rpt_family="Alu"
complement(18270..18438)
/notes="predicted exon, program: grill2exons_human_1.3,
frame: 0, quality: excellent, score:
100.000--(18438..18284) DSS similarity to
mel7b11.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus
cDNA clone 387741 5' similar to PIR:B38252 B38252
granulocyte colony-stimulating factor receptor precursor
(157..1); 82% identity.--(18438..18406) DSS similarity to
AA049280 mJ45d02.r1 Soares mouse embryo NBME13.5 14.5 Mus
musculus cDNA clone 479043 5' similar to SW:IL6B_MOUSE
Q00560 INTERLEUKIN-6 RECEPTOR BETA PRECURSOR (432..464);
88% identity."
complement(18540..18697)
/notes="predicted exon, program: grill2exons_human_1.3,
frame: 1, quality: excellent, score: 100.000--DDS
similarity to W66776 mel7b11.r1 Soares mouse embryo
NBME13.5 14.5 Mus musculus cDNA clone 387741 5' similar to
PIR:B38252 B38252 granulocyte colony-stimulating factor
receptor precursor (316..158); 92% identity.--DDS
similarity to AA049280 mJ45d02.r1 Soares mouse embryo
NBME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to
SW:IL6B_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN
PRECURSOR (274..431); 93% identity.--"

```

Query Match

23.8%; Score 331; DB 11; Length 40668;

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QY 1091 aggcgaaccccaaaatgggccacctctgtacctacttcagggaacctgagc--ccct 1148
Db 15169 AGGCGRACCCAACTAGGGCCACCTCTGTACCTCTACTTCAGGGCACCTGAGCCACCT 15110

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Db 15109 CAGCAGAGCTGGGGTGGCCCTGAGCTCCACGCCATACAGCTCTGACTCCACGTG 15050

QY 1209 aggcacatttgggtgacccccagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtg 1268
Db 15049 AGGCACCTTTGGTGGTCCACCCAGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 14990

QY 1269 cctagaacctctccagggctgggggtgagaaagggagtcattactccccattacacagg 1328
Db 14989 CCTAGAACCCTCTGCCAGGGGTGGGGGTGAGAAGGGGAGTCATTACTCCCATACCTAGG 14930

QY 1329 gccctccaaaagagtcctctttaataaatgagctatttaggtgc 1373
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RESULT 9
LOCUS A70386 938 bp DNA PAT 07-MAY-1999
DEFINITION Sequence 16 from Patent WO98111225.
ACCESSION A70386
NID 94774665
VERSION A70386.1 GI:4774665
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 938)
AUTHORS Nicola.N.A., Fabri,L., Farley.A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
TITLE A NOVEL HEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME.
JOURNAL Patent: WO 9811225-A 19-MAR-1998;
NICOLA NICOS ANTONY (AU)
FEATURES
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ORIGIN

Query Match 18.0%; Score 249.8; DB 5; Length 938;
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Matches 275; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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VERSION A70388.1 GI:4774667
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 834)
AUTHORS Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S., Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and Kikuchi, Y.
TITLE A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
JOURNAL Patent: WO 9811225-A 19-MAR-1998;
NICHOLA NICOS ANTONY (AU)
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Best Local Similarity 87.7%; Pred. No. 2.2e-107;
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DB 148 GCCTGGCCCTGGCTAACCTTATGGGTCCAGGCACAGTCAGGAGACAACTCGGTGTGT 207
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RESULT 7
A70393
LOCUS A70393 560 bp DNA PAT 07-MAY-1999
DEFINITION Sequence 23 from Patent WO9811225.
ACCESSION A70393
NID 94774671
VERSION A70393.1 GI:4774671
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 560)
AUTHORS Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S., Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and Kikuchi, Y.
TITLE A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
JOURNAL Patent: WO 9811225-A 19-MAR-1998;
NICHOLA NICOS ANTONY (AU)
FEATURES
source Location/Qualifiers
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Best Local Similarity 99.6%; Pred. No. 3.4e-99;
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Matches 1368; Conservative 0; Mismatches 0; Indels 7; Gaps 2;
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DB 1662 ATTACTAGGGCCCTCCAAAAGAGTCTTTAAATAAATAGACTATTATTAGGTGC 1716

RESULT 3
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LOCUS
DEFINITION
Sequence 14 from Patent WO9811225.
ACCESSION
A70384
NID
94774664
VERSION
A70384.1
GI:4774664
KEYWORDS
unidentified.
SOURCE
unidentified.
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 1673)
AUTHORS
Nicola N.A., Fabri L., Farley A., Nash A., Willson T., Rakar S.,
Zhang J., Alexander W., Hilton D.J., Kojima T., Maeda M. and
Kikuchi Y.

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BASE COUNT 281 a 459 c 417 g 234 t

ORIGIN

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Query Match 100.0%; Score 1391; DB 5; Length 1391;
Best Local Similarity 100.0%; Pred. No. 2.1e-261;
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RESULT 2

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LOCUS Homo sapiens cytokine-like factor-1 precursor (CLF-1) mRNA, complete cds.

DEFINITION AF059293

ACCESSION AF059293

NID 93372626

VERSION AF059293.1 GI:3372626

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

REFERENCE 1 (bases 1 to 1716)

AUTHORS Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE Elson, G.C.A., Graber, P., Losberger, P., Herren, S., Gretener, D.,

JOURNAL Menoud, L.N., Wells, T.N.C., Kosco-Vilbois, M.H. and Gauchat, J.F.

REFERENCE CLF-1, a Novel Soluble Protein Shares Homology With Members of the

AUTHORS Cytokine Type-I Receptor Family

JOURNAL J. Immunol. (1998) in press

REFERENCE 2 (bases 1 to 1716)

AUTHORS Elson, G.C.A., Graber, P., Losberger, P., Herren, S., Gretener, D.,

TITLE Menoud, L.N., Wells, T.N.C., Kosco-Vilbois, M.H. and Gauchat, J.F.

JOURNAL Direct Submission

REFERENCE Submitted (14-APR-1998) Dept. of Immunology, Sero-pharmaceutical

FEATURES Research Institute, 14, Chemin des Aulx, Plan-les-Ouates, GE 1228, Switzerland

LOCATION/Qualifiers

1. 1716 /organism="Homo sapiens"

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DPQLALTAVQVRVLEVEVQEVAKARLPDNRVLYIETASADETDASDENEEAAK

6210. .6215

/gene="SC9B10.04"

Query Match

Best Local Similarity 3.4%; Score 47.8; DB 1; Length 33320;

Matches 205; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

Qy 492 cgtgcacgtgagccgcgtgcgggctggaggaccagctgagcgtgctgggtgcgc 551

Db 14709 CGGCGACGTCGGCCACGTCGACCGGCTCGTCCAGCGCTCGCGAGCAGCTGCCGCCG 14768

Qy 552 accgcccctcaagattctctcttcaagcaaataccagatccgtaccagtgaggga 611

Db 14769 CAGCGCCCTGTAGCTCACCGCCGACCGCATGGTCGACGTGCCCTTCGACGAGGACA 14828

Qy 612 cagtgtggactggaagtggtgagcatgtgagcaaccagacctctcgcgcctggccgg 671

Db 14829 CCGGATCGACTTCGACGAGGACTGGGAGCTGAAGCGGGCGTCCCTCTCGCGGCGCA 14888

Qy 672 cctgaaccccgccacgtgtactctgcaagtgcgtgcaaccccttggcatctatgg 731

Db 14889 GGGCCGCGCCGCGACGTCTAGCGCGTCCCGCGCGCGACGACGCTGCTTCTGCTG 14948

Qy 732 ctccaagaagccgggactctgagtgagtgagtgagccaccacagccgcctccactccc 791

Db 14949 GCGCGAGGTGCTCGCGAGCAGTCTCTGGTGCGGTCCCGGAGGCGGATCGCCCGCG 15008

Qy 792 cagtgc 851

Db 15009 CTGGTTCGCCGCCGGTATCGACGACGCGGTGTACGACCGCATCGCGAGCTGGTCGCCG 15068

Qy 852 ggggcccgtgc 911

Db 15069 GCGCCGCGACGACGTCCTGGTCTATCGCCTCCAGCGCGAGCCCAAGGATCGCGCGATGT 15128

Qy 912 ctccaacctcagcttcgcctctacgaccagtggcgagcctggatgc 958

Db 15129 CGGCAACACACGTTGATGACCCCTGCCGAGCAGCTCGTCCCGCTGC 15175

Search completed: September 28, 1999, 16:40:47
Job time: 7034 sec

Query Match 57.5%; Score 799.4; DB 1; Length 1629;
 Best Local Similarity 87.8%; Pred. No. 1.4e-159;
 Matches 872; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 1 accctcaacggcgccgctgccccctgaagctctcccggtgtactcaacgccccacccttg 60
 DB 361 ACCCTCAATGTCGCGCGCTGCCCTGAGCTGTCCGGCTCTTAACACCTCCACCCCTG 420
 QY 61 gctctggccctggcccaacctcaaatgggtccagcagcgtcgggggagacacacctgtgtgc 120
 DB 421 GCCCTGGCCCTGGCTTAACCTTAATGGGTCCAGCAGCAGTCCAGGAGACAATCTGTGTGT 480
 QY 121 cagcccgtagcgcagcatcctgctggctcctcctctctctatgttgctgccccagag 180
 DB 481 CAGGCCGAGACGGCAGCATCTGCTGGCTGCTCTCTCTATGTGTGGTGGCTGCCCTGAG 540
 QY 181 aaacccgtcaacatcagctgctgggtcccaagaacatgaagactgaacctgcgcgtggagc 240
 DB 541 AAGCCCTTAACATCAGCTGCTGGTCCCGGACATGAAGGATCTCACGTGGCGCTGGACA 600
 QY 241 ccaggggccccacgggagacctctctccacacacactactcctcaagtacaagcttagg 300
 DB 601 CCGGGTGACACGGGGAGACATCTTACATACCACTACTCCCTCAAGTACAGCTGAGG 660
 QY 301 tggtagccagggacacacacatgtgaggagtaccacacagtgggggccccactctgtccac 360
 DB 661 TGGTACGCTCAGGATAACACATGTGAGGAGTACCACACTGTGGGCCCTCACTCATGCCAT 720
 QY 361 atccccaggacctggctctctttacccctctatgagatcttggtggggggccacacacgcg 420
 DB 721 ATCCCCAAGNACCTGGCCCTCTTACCTCCCTATGAGATCTGGGTGGAGCCACCAATGCC 780
 QY 421 ctgggtctctccgctccgactgactacgctggtatctctctggtggtggggccccactctgtcc 480
 DB 781 CTAGGCTCAGCAAGATGTGTCTCTCACACTGGATGTCTCTGGACGTGGTGGACCGGAC 840
 QY 481 cccccggcagctgacgtgagccgctgctggggggcctggaggaccagctgagctggcgc 540
 DB 841 CCCCCACCCGACGTGCAGTGCAGTGGCGGCTGGGGGCTGGAGGACCACTGAGTGGCGC 900
 QY 541 tgggtgcgcaccccgccctcaaggattctctcttcaagcccaataccagatccgctac 600
 DB 901 TGGGTCTACACACAGCTCTCAGAGATTTCTCTTCCAAAGCCAAAGTACCAGATCCGCTAC 960
 QY 601 cgagtgaggacagctgtgagctgaaagtggtgagcatgtgagcaaccagacctctgc 660
 DB 961 CGCGTGGAGACAGCTGGACTGGAAGTGTGTGATGACGTCAACCAACCAAGACCTCCTGC 1020
 QY 661 cgctggcgccctgaaacccggcaccgctgactctgtgcaagtgcgctgcaaccccttt 720
 DB 1021 CGTCTCGCGGGCTGAAGCCCGCACCGTTTACTTCTGTCAGTGGCTTTTACCCATTC 1080
 QY 721 ggcattctatgctccaaagaacgcgggactgagtgagtgagtgaggccaccacagcgcc 780
 DB 1081 GGGATATGGGTGCGAAAGAGCGGGAATCTGGAGCGAGTGGAGCCACCCACCGCTGCC 1140
 QY 781 tcaactccccgagtgagcgccggcgccggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 840
 DB 1141 TCCACCCCTCGAAGTACGCGCCCGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
 QY 841 gagccgagctcgggcgctgagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 900
 DB 1201 GAGCCACGCTCGGGCCCGTGGCGCGGAGCTCAACGAGTTCCTCGGCTGGCTCAAGAAG 1260
 QY 901 cagcgtagctctcaacctagcttccgctctacgaccagtggcgagcctggatgcag 960
 DB 1261 CAGGCATATGCTCGAACCTTATGTTCCGCTCTACGACCAAGTGGGTGTGTGGATGCGAG 1320
 QY 961 aagtcgcaagacccgcacacagcagagc 993
 DB 1321 AAGTCACACAGACCCGAAACCAAGCGTCTGCCG 1353

RESULT 10
 V27143
 ID V27143 standard; cDNA; 834 BP.
 AC V27143;
 DT 29-SEP-1998 (first entry)
 DE Nucleotide sequence of products generated by 5N race of brain cDNA.
 KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
 KW cell survival; therapeutic; neuronal proliferation; drug screening; ss;
 OS Mouse.
 FT Mus sp.
 FT Key
 FT CDS
 Location/Qualifiers
 1..834
 /*tag= a
 /product= "Haemopoietin receptor"
 PN W09811225-A2.
 PD 19-MAR-1998.
 PF 11-SEP-1997; G02479.
 PR 11-SEP-1996; AU-002246.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA (DZIE/) DZIELENSKA H E.
 PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
 PI Zhang J;
 DR WPI; 98-260970/23.
 DR P-PSDB: W55014.
 PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PT e.g. neuronal cells
 PS Claim 7; Page 93-95; 182pp; English.
 CC The nucleotide sequence was generated by a 5N RACE of brain cDNA using
 CC NR6 specific primers. NR6 is a novel Haemopoietin receptor (HR).
 CC Interaction between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and it's
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 834 BP; 167 A; 274 C; 225 G; 168 T;

Query Match 43.0%; Score 598.8; DB 1; Length 834;
 Best Local Similarity 87.7%; Pred. No. 1.7e-117;
 Matches 654; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 1 accctcaacggcgccgctgccccctgaagctctcccggtgtactcaacgccccacccttg 60
 DB 88 ACCCTCAATGTCGCGCGCTGCCCTGAGCTGTCCGGCTCTTAACACCTCCACCCCTG 147
 QY 61 gctctggccctggcccaacctcaatgggtccagcagcgtcgggggagacacacctcgtgtgc 120
 DB 148 GCCCTGGCCCTGGCTTAACCTTAATGGGTCCAGCAGTCCAGGAGACAATCTGTGTGT 207
 QY 121 cagcccgtagcgcagcatcctgctggctcctcctctctatgttgctgccccagag 180
 DB 208 CAGCCCGAGACGGCAGCATCTGGCTGGCTCTCTCTCTATGTGTGGCTGCCCTGAG 267
 QY 181 aaacccgtcaacatcagctgctgggtcccaagaacatgaagacttgacctgcgctggagc 240
 DB 268 AGCCCTTTAATCATCAGCTGCTGGTCCCGGAACATGAAGATCTCACGTGGCGCTGACA 327
 QY 241 ccagggggccacaggggagaccttcccccacacactactcctcaagtacaagcttagg 300
 DB 328 CCGGGTGACACGGGGAGACATCTTACATACCACTACTCCCTCAAGTACAGTGGAG 387
 QY 301 tggtagccagggacacacacatgtgaggagtaccacacagtgggggccccactcctggcac 360
 DB 388 TGGTACGCTCAGGATAACACATGTGAGGAGTACCACACTGTGGGGCCCCCNCATGCCAT 447
 QY 361 atccccaggacctggctctctttacgccccctatgagatgtggtggagcccaaccgcg 420
 DB 448 ATCCCCAAGGACCTGGCCCTCTTACTCCCTATGAGATCTGGTGGAGCCCAACCAATCGC 507

QY 421 ctgggtctgcccgcctccgatgtactacagctggtatctctggtggtggtaccagcagc 480
Db 816 CTGGGTTCACGAGAGATCTACGTCGTCACACATGGATGCTCTGAGCAGTGTGACACGGAC 875
QY 481 ccccccgcagcagctgacgtgagccgctgctgggggctgagagaccagctgagcgtgcgc 540
Db 876 CTTCCACCCGACGTGACGTGAGCCGCTGGGGCTGGAGACACAGCTGAGTGTGCGC 935
QY 541 tgggtgtccaccgcccccctcaaggatttctcttcaagcccaataccagatccgctac 600
Db 936 TGGGTCTCACACACAGCTCTCAAGGATTTCTCTTCCAAAGCCAAATACAGATTCGCTAC 995
QY 601 caagtggagacagtgtgactgagagagtggtgagcagatgtgagcaacagaccctctgc 660
Db 996 CGGTGGAGACACGTGGACTGGAGGTGGTGGATGAGCTGACGACCAACAGACCTCTCTGC 1055
QY 661 cgctggcgccctgaacccgcagcctgtactctgctcaagtgcgtgcgaaccccttt 720
Db 1056 CGTCTCGGGGCTTGAAGCCGCGCACCGTTTACTTCTGTCCAAGTTCTGTTGTAACCCATTC 1115
QY 721 ggcattatggctccaaagacgagcgtggtgagtgagtgagtgagcagcccccagcgcgc 780
Db 1116 GGGATATATGGTTCGAAAGAGCGGGAATCTGGAGCGAGTGGAGCCACCCACCGCTGCC 1175
QY 781 tccactcccgagtgagc 840
Db 1176 TCCACCCCTCGAAGTGAAGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1235
QY 841 gagcagagctcgggcggtgc 900
Db 1236 GAGCCTAGCTCGGCGCGGTGCGCGCGAGCTCAAGCAGTTCTCGGCTGGCTCAAGAAG 1295
QY 901 caagcgtactgtctcaacctcagcttcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 960
Db 1296 CAGCGTACTGCTCGAACCCTAGCTTCGCGCTGTACGACGAGTGGCTGTGATGCGAG 1355
QY 961 aagtcgcaagacccgcaacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1020
Db 1356 AAGTCACACAGACCCCGAAGC-----CAGGACGAGGGGATCTCGCCCTCGGGGACAGCGG 1410
QY 1021 gcacggcgagaggtccctgcagataaagctgtgaggggtcagggccacccctccctgccacgt 1080
Db 1411 GTGCGGCGAGAGTCTCTCGCGCTAACTCTGAGG---ATAGGCCATCTCTCTGCTGAT 1467
QY 1081 ggagacgagagggcgcaaccccaactggggccacctctgtacccctcaacttcaggggacct 1140
Db 1468 GCAGACCTGGAGGCTACCTGAACTGGAGACCA--TCTGTACTGTCACTTTGGGGCAATG 1525
QY 1141 gagccctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1163
Db 1526 AAGAAACAAACCGGGGCTGGGG 1548

RESULT 6

V27141
ID V27141 standard; cDNA; 1673 BP.
AC V27141;
DT 29-SEP-1998 (first entry)
DE Novel haemopoietin receptor NR6.2 gene.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening; ss;
KW Mouse.
OS Mus sp.
FH key
FT CDS
FT Location/Qualifiers
1..1278
/tag- a
/product- "Haemopoietin receptor NR6.2"
FN W09811225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIE/) DZIELEWSKA H E.

PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
PI Zhang J;
DR WPI; 98-260970/23.
DR P-PSDB; W55012.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PS Claim 5; Page 84-87; 182pp; English.
CC The haemopoietin receptor (HR) NR6.2 is a form of the novel HR NR6.
CC interaction between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and its
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SQ Sequence 1673 BP; 344 A; 550 C; 474 G; 305 T;

Query Match 60.1%; Score 836.6; DB 1; Length 1673;
Best Local Similarity 87.8%; Pred. No. 2.1e-167;
Matches 926; Conservative 0; Mismatches 124; Indels 5; Gaps 1;

QY 1 accctcaacggcgccgctgccccctgagctctccctgtactcaacgcctccaccttg 60
Db 362 ACCCTCAATGGTGGCGGCTGCCCTCTGAGCTGTCCCGCTCTTAAACACTCCACCTG 421
QY 61 gctctggcctggcgaacactcaatgggtccaggcagcgtgcgggggacaaactcgtgtgc 120
Db 422 GCCCTGGCCTGGCTAAACCTTAATGGGTCCAGGACGACGAGGACAACTCTGGTGTG 481
QY 121 cagcccgctgagcggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
Db 482 CAGCGCCGAGAGCGGAGCAGCTTGGCTGCTCTGCTCTCTATGTTGGCTGGCCCTGAG 541
QY 181 aaaccgctcaacatcagctgctggtccaaagacatgaagactgagcctgagcagcagc 240
Db 542 AAGCCCTTAAACATAGCTGCTGGTCCCGAAGATGAAGATCTACGTCGCCCTGGACA 601
QY 241 ccaggggccacggggagagccttccctccacacaaactactccctcaagtacagcttagg 300
Db 602 CCGGGTGCACAGGGGAGACATCTTACATACCACTACTCCCTCAAGTACAGCTGAGG 661
QY 301 tggatggccagacacacacatgtaggagtagcaccacagtgaggggcccaactcctgccac 360
Db 662 TGGTACGCTCAGGATAACACATGTGAGAGTACACACTGTGGGCGCTCCTCCTCATGCT 721
QY 361 atcccaaggacgtgctctcttaccgcttatgagctgagtgagggcagccacacacgc 420
Db 722 ATCCCAAGGACCTGGCGCTCTTCACTCTCTATGAGATCTGGGTGAAGCCACCAATCGC 781
QY 421 ctgggctctgcccgtccgatgtactcaagctggtatctcctggtatggtgacacagcagc 480
Db 782 CTAGGCTCAGCAAGATCTGTATGCTTCACACTGGATGCTCTGGAGCTGTGACACGGAC 841
QY 481 ccccccccgacgtgacgtgagc 540
Db 842 CCCCCACCCGACGTGACGTGAGCCGCTGGGGGCTGGAGGACGAGCTGAGTGTGCGC 901
QY 541 tgggtgtgcccaccccgccctcaaggatttctcttcaagcccaataccagatccgctac 600
Db 902 TGGGTCTCACACACAGCTCTCAAGGATTTCTCTTCAAGCCAAAGTACCAAGATCCGCTAC 961
QY 601 cgagtggagacagtggtgagtgagtggtgagtgagtgagtgagtgagtgagtgagtgag 660
Db 962 CGCGTGGAGGACAGCGTGGACTGGAGGTGGTGGATGACGTGACGACCAACGAGACCTCT 1021
QY 661 cgctgcccgcctgaacccgcagcagcagcagcagcagcagcagcagcagcagcagcagc 720
Db 1022 CGTCTCGGGGCTGAAGCCGCGCACCGTTTACTTGTGTCACAGTGGCTTGAACCCATTC 1081

QY 421 ctgggctctgcccgtccggtgactcaagctggatattctctgagatgtgtgacacggac 480
 Db 608 CTGGGCTCTGCCGCTCCGATCTACAGCTGGATATCTCTGGATGTGTGACACGGAC 667
 QY 481 ccccgccgagctgacgtgagcgcgctcgggccctggagacagctgagctgagcgc 540
 Db 668 CCCCCCGCGAGCTGACGTGAGCCGCTCGGGGCGCTGGAGACAGCTGAGCTGGCG 727
 QY 541 tgggtgtgcacccgcccctcaagattctctcttcaagccaaataccagatccgctac 600
 Db 728 TGGGTGTGCCACCCGCTCAAGGATTTCTCTTTCAAGCCAAATACAGATCCGCTAC 787
 QY 601 cgagtggagacagctgtgactggaagtgtgtgacgatgtgagcaaccagacctctgc 660
 Db 788 CGAGTGGAGGACAGTGTGGATGTGAAGTGTGGACGATGTGAGCAACACAGACCTCTGC 847
 QY 661 cgcctggcgcgcctgaacacccgacccgtgactcttgcgaagtgcgtgcaacccttt 720
 Db 848 CGCTGGCGCGCTGAACCCCGCACCGCTGACTTGTGTGCAAGTGGCTGCAACCCCTT 907
 QY 721 ggcattctatgctcacaagaacgggagctctggagtgagtgagagccaccacagccgc 780
 Db 908 GGCATCTATGCTCCAGAAAGCGGGATCTGGAGTGAAGTGGAGCCACCCACAGCCGCC 967
 QY 781 tccactcccgcagtgagc 840
 Db 968 TCCACTCCCCAGTGAAGCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1027
 QY 841 gagcgcagctggcgccgctgagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 900
 Db 1028 GAGCGGAGCTCGGGCGCGCTGCGCGCGAGCTCAAGCAGTTCCTTGGGTGGCTCAAGAAG 1087
 QY 901 caecgctactgctcacaacctcagctccgctctacagaccagtgagcgcgcgcgcgcgcgc 960
 Db 1088 CACGCTACTCTCTCAACCTCAGCTTCGCTCTACGACGAGTGGCGAGCTGTGATGCG 1147
 QY 961 aagtcgacagaaccccaaccacagcagcagcagcagcagcagcagcagcagcagcagc 1020
 Db 1148 AAGTCGCACAGACCCCGCAAC-----CAGGACGAGGGGATCTCTGCCCTGGGCGACGCGG 1202
 QY 1021 gcacggcgagaggtcctgcccagataaagctgtaggggtcagggccaccctccctccacgt 1080
 Db 1203 GCACGGCGAGAGGTCTCGCAGATAAGCTGTAGGGGCTCAGGCCACCTCTCCTGCCACGT 1262
 QY 1081 ggagacgagagggcggaacccaaactgggcacactctgtaccctcacttcagggaacct 1140
 Db 1263 GGAGACGACAGGCGCGACCCAACTGGGGCCACCTCTGTACCTCACTTCAGGGCACCT 1322
 QY 1141 gacg--ccctcagcagagctgggtggccctgagctccaaacggccataaacagctctga 1198
 Db 1323 GAGCCACCTTCAGCAGGAGCTGGGTGGCCCTGAGCTCCAAACGGCCATTAACAGCTCTGA 1382
 QY 1199 ctcccagctgagccaccttgggtgaccccaagtggtgtgtgtgtgtgtgtgtgtgtgtgt 1258
 Db 1383 CTCCACGTGAGGCGCACCTTGGGTGACCCCACTGAGTGGGTGTGTGTGTGTGTGTGTGTGT 1442
 QY 1259 ggttggcttcctagaaacccctgacagggctgggggtgagaagggagcttactctccc 1318
 Db 1443 GGTGTAGTTCCTAGAACCCCTGCCAGGGCTGGGGGTGAGAAGGGGAGTCATTACTCCCC 1502
 QY 1319 attactagggccctcccaaaagctctttaaataaatgagctatttaggtgcaaaaa 1378
 Db 1503 ATTACCTAGGGCCCTCCAAAGAGTCTTTTAAATAAATGAGCTATTTAGGTGCTGTGA 1562
 QY 1379 aaaaaaaaaa 1391
 Db 1563 AAAAAAAAAA 1575

RESULT 5
 V70896
 ID V70896 standard; cDNA; 1724 BP.

AC V70896;
 DT 17-MAR-1999 (first entry)
 DE cDNA encoding rat Zcytor5.
 KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; Zcytor5 ligand; ss.
 OS Rattus sp.
 FH Key
 FT Location/Qualifiers
 FT 159..1436
 FT /*tag= a
 FT /product= zcytor5
 PN W08949307-A1.
 PD 05-NOV-1998.
 PE 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI; 99-034662/03.
 DR P-PSDB; W70862.
 PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
 PT down-regulating Zcytor5 natural ligands or detecting cardiostrophin-1
 PT in blood
 PS Disclosure; Page 72-75; 55pp; English.
 CC The present sequence encodes a protein designated Zcytor5, which is
 CC a cytokinin-like receptor. Soluble Zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytor5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible Zcytor5 ligands. A probe
 CC comprising Zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytor5 and
 CC therapeutically to modify Zcytor5 ligand effects.
 SO Sequence 1724 BP; 350 A; 550 C; 324 T;

Query Match 60.9%; Score 847.4; DB 1; Length 1724;
 Best Local Similarity 84.9%; Pred. No. 1.1e-169;
 Matches 987; Conservative 0; Mismatches 166; Indels 10; Gaps 3;

QY 1 acctcaacggcgccgctgcccctgagctctccgtgactccggtactcaacgctccacttg 60
 Db 396 ACCCTCAACGGCGCGCTGCCCTCAGAGCTGCCGCTCTCTCAACACCTCCACCTTG 455
 QY 61 gctctggccctggccaaactcaatgggtccaggcagcgtcgggggacacactcgtgtgc 120
 Db 456 GCCTTGGCCCTTGCTTAACCTTAATGGGTCCAGGCAGTCAGGGGACAACTCTGGTGT 515
 QY 121 cagcgccgtgacgcagcagcctcgtggtgctcctgctctatgttgctgccccagag 180
 Db 516 CAGCGCCGAGATGGCAGCATTTGGCTGGTTCTCTATGTGTGTCTGCCCGGAG 575
 QY 181 aaaccgctcaacatcagctgctggtccaaagaacatgaaggacttgacctgacctgagc 240
 Db 576 AAGCCCTTTAATCATCAGCTGCTGGTCCCGGACATGAAGAGCTGACATGCCGTGGACA 635
 QY 241 caagggggccaggggagacctctcccaacaaactcctcccaagtacaagcttagg 300
 Db 636 CCGGGTGCATCGGGGAGACATTCCTTACACACCACTACTCCTCAAGTACAAGTGAAG 695
 QY 301 tggatgcccagagacacacatgtgagagtagccacacagtgggggccactccctgcaac 360
 Db 696 TGGTATGGTCAGGACAAACATGTGAGGAATATCATCTGTGGGCCCTCCTCCTGCTCAT 755
 QY 361 atccccaaagacgtggtctctttacgcccctatgagctggtgagggccacacacgc 420
 Db 756 ATCCCCAAGACCTGGCCCTCTTCACGCCCTATGAGTCTGGGTGGAAGCCCAATCGC 815

Db 580 TGGTATGCCAGGACACACATGTAGAGGATACACACAGTGGGGCCCCCCTCTCTGCGCAC 639
Qy 361 atccccaaagacgtggtctctttacccctatgagatctgggtggagggccacacacgc 420
Db 640 ATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGATCTGGGTGGAGGCCACCAACCGC 699
Qy 421 ctgggtctgccccctccgatgtactcaacgctgatactcctggatgtgtgtgacacggac 480
Db 700 CTGGGCTCTGCCCTCCGATGTACTACGCTGATATCTCTGGATGTGTGGTGGACACCGAC 759
Qy 481 cccccccacagtgacgtgagccgctggggcctgaagacacagctgagcgtgcgc 540
Db 760 CCCCCCGGCAAGTGCACGTGAGCGGCTGGGGGCTGGAGGACCACTGAGGCTGCGC 819
Qy 541 tgggtgtgcacccgcctcaagattctcttcaagcacaataccagatcgcgtac 600
Db 820 TGGGTGTGCGCACCGCCCTCAAGGATTTCTCTTTCAAGCAATACAGATCCGCTAC 879
Qy 601 cagtgagagacagtgtgactggaagtggtgagacagtgtgagcaacacacacacac 660
Db 880 CGAGTGGAGGACAGTGTGGACTGGAAGTGTGGACGATGTGAGCAACCAACGACCTCTG 939
Qy 661 cgcctgcccgcctgaaacccgacacgctgactctgcaagtgcgtcgaaccccttt 720
Db 940 CGCTGGCGGCTTGAACCCGACCGCTGTACTTCTGCAAGTGCCTGCAACCCCTTT 999
Qy 721 ggcactatggtctcaagaagacgggactctggagtgagtgagcaccacacacacgcgc 780
Db 1000 GGCATCTATGCTCCAGAAAGCCGGATCTGGAGTGGAGTGGAGCCACCCACAGCCGCC 1059
Qy 781 tccactcccagtgagccgcccggccggccggccggccggccggccggccggccggcc 840
Db 1060 TCCACTCCCCAGTAGAGCGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGG 1119
Qy 841 gagcgaagctcggggcgggtgcgcgagctcaagcagttcctgggctggctcgaagaag 900
Db 1120 GAGCGAGCTCGGGCCGGTGGCGGAGCTCAAGCAGTTCTTGGGCTGCTCAAGAAG 1179
Qy 901 cagcgtactgtccaaactcagcttcgcctctacacacagtgagcagcgtgagtcag 960
Db 1180 CACGGTACTGCTCCAACTCAGCTTCGGCTCTACGACCAAGTGGCGAGCCTGATCAG 1239
Qy 961 aagtcgacaaagacccgcaacacagcagcagcagcagcagcagcagcagcagcagc 1020
Db 1240 AAGTGCACAAAGACCCGCAAC-----CAGGACGAGGGGATCTCTCCCTCGGGCAGACGG 1294
Qy 1021 gcagcgcagaggtctctccagataagctgtagggctcagggccacacccctccctccacgt 1080
Db 1295 GCACGGCAGAGGTCTCTCCAGATAAGCTGTAGGGCTCAGGCCACCCCTCCCTGCCACGT 1354
Qy 1081 ggagcgcagagggccgaacccaaactggggccacctctgtacctcacttcaggggcacct 1140
Db 1355 GGAGACGAGAGGGCCGAACCCAACTGGGGCCACCTCTGTACCTCTCATTTCAGGGCACCT 1414
Qy 1141 gaggc---cctcagcagagagctgggggtggccctcagctcccaacggccatacagctctga 1198
Db 1415 GAGCCACCTCAGCAAGAGCTGGGTGGCCCTCAGCTCCCAACGCCCATACAGCTCTGA 1474
Qy 1199 ctccacagtgagccaccttgggtgacccccagtggtgtgtgtgtgtgtgtgtgtgtgt 1258
Db 1475 CTCCACAGTGAGGCCACCTTTGGGTGCACCCAGTGGGTGTGTGTGTGTGTGTGTGTGT 1534
Qy 1259 ggttgagtgctagaacccctgcccagggctgggggtgagaggggaggtcattactcccc 1318
Db 1535 GTTGTGAGTTGCTAGAACCCCTGCCAGGGCTGGGGGTGAGAGGGGAGCTATTACTCCCC 1594
Qy 1319 attactaggccctcccaagagctccttttaataaataagctatttaggtgcaaaaa 1378
Db 1595 ATTACTAGGGCCCCCTCCAAAAGAGTCTCTTTAAATAATGAGCTATTATTAGGTGCAAAA 1654
Qy 1379 aaaaaaaaaa 1391
Db 1655 AAAAAAAAAAAAAA 1667

RESULT 4

V41689
ID V41689 standard; cDNA; 1579 BP.
AC V41689;
DE 26-OCT-1998 (first entry)
KW Human; U4 protein; haematopoietin receptor superfamily;
KW cell proliferation; immune response; antibody; cell differentiation;
KW autoimmune disease; cancer; allergy; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT 1..1228
FT CDS /tag= a
FT /product= "U4 protein"
WO9831811-A1.
23-JUL-1998.
PF 15-JAN-1998; U00334.
PR 16-JAN-1997; US-784863.
PA (GEM) GENETICS INST INC.
PI Collins M, Donaldson DD, Neben T, Whitters M;
DR WPI: 98-414109/35.
DR P-PSDB; W59805.
PT New nucleic acid encoding U4 haematopoietin receptor superfamily
PT chain - potentially useful, e.g. for modulating cell proliferation
PT or immune response, for treating cancer and auto-immune disease
PS Claim 1: Page 28; 38pp; English.
CC This is the nucleotide sequence encoding the human U4 protein from
CC the haematopoietin receptor superfamily, used in the method of the
CC invention for the modulation of cell proliferation, or the immune
CC response. Transformed mammalian cells are used to produce recombinant
CC U4 protein. The U4 protein is used to screen for specific binding
CC agents, raise antibodies. It is also used as reagents for assays and
CC as tissue markers for isolation of cognate ligands and receptors and
CC in pharmaceutical compositions which may modulate cell proliferation,
CC cell differentiation, and the immune system (e.g. for treating immune
CC deficiency, inherited, or the result of infection, autoimmune diseases,
CC cancer, and allergy).
SQ Sequence 1579 BP; 304 A; 535 C; 473 G; 267 T;

Query Match 97.2%; Score 1352.6; DB 1; Length 1579;

Best Local Similarity 99.2%; Pred. No. 8.3e-276;

Matches 1382; Conservative 0; Mismatches 4; Indels 7; Gaps 2;

Qy 1 accctcaagggcgccgctgccccctgagctctccgtgtactcaacgctccaccttg 60

Db 188 ACCCTCAACGGGGCGCGCTGCCCCCTGAGCTCTCCGCTACTCAACGGCTCCACCTTG 247

Qy 61 gctctggccctggcccaacctcaatgggtccagcagcggctcggggacacacccctgtgc 120

Db 248 GCTCTGGCCCTGGCCCAACCTCATGGTCCAGCAGGGTTCGGGGACACCTCTGTCG 307

Qy 121 cagcgcggtgacggcagcagctcctgggtggtcctgctctatgttggcctgccccacag 180

Db 308 CAGCGCCGTGACGGCAGCATCTCTGGTGGCTCTGCTCTCTATGTGGCTGCCCCACAG 367

Qy 181 aaacccgtcaaatcagctgctggtccaagaacatgaagacactgacctgcgctgacg 240

Db 368 AAACCCGCTCAACATCAGCTGCTGTGTCACGAAGATGAAGACTTGACCTCCCGCTGACG 427

Qy 241 ccagggggccacggggagagccttctccacacacacacacacacacacacacacacac 300

Db 428 CCAGGGGCCCCACGGGGAGACCTTCCCTCCACACCACTACTCCCTCAAGTACAGCTTAGG 487

Qy 301 tgggtatggccagac 360

Db 488 TGGTATGGCCAGGACACACACATGTGAGGAGTACCACACAGTGGGGCCCCCCTCTGTCG 547

Qy 361 atccccaaagacgtgctctctttagccctatgagatctgggtggagggccacacacgc 420

Db 548 ATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGATCTGGGTGGAGGCCACCAACCGC 607

Db 301 TGGTATGCCAGGACAAACATATGTAGAGATACACACATGGGGCCCCACTCTGCGAC 360
Qy 361 atccccaaagacgtgctctcttttacgccttatgagatctgggtggggccaccacgc 420
Db 361 ATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGATCTGGGTGGAGGCCACCAACCGC 420
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Qy 481 ccccgccacagtgacgtgacgcgtgagggcgctgagggcctgagggcagcagcgtgcgc 540
Db 481 CCCCCTGCCGACGTGACGTAGCGCGCTCGGGGGCTTGGAGGACCACTGAGCGTGC 540
Qy 541 tgggtgtgcacccgcctcaagattctctcttcaagccaaataccagatccgctac 600
Db 541 TGGGTGTGCGCACCGGCCCTCAAGGATTTCTCTTTCAAGCCAAATACAGATCCGCTAC 600
Qy 601 cagtgaggagacagtgtgactggaaggtggtgacatgtgagcaacacagacctctgc 660
Db 601 CGAGTGGAGGACAGTGTGAGTGAAGGTGTGGACGATGTGAGCAACACGACCTCTGCG 660
Qy 661 cactgcccgcctgaaccgacagctgactctgagagtcgagtcgacgtgacacccctt 720
Db 661 CCGCTGGCGGCTGAACCCGCGACCGGTGACTGTGTCGCAAGTGGCTGCAACCCCTTT 720
Qy 721 ggcattatggtctcaagaagcggtgactgagtgagtgagtgagcaccacacagcgcc 780
Db 721 GGCATCTATGCTCCAAAGACCGGGATCTGGAGTGTGAGTGAGGACCCACAGCGCC 780
Qy 781 tccactccccagtgagcgccggccggcgccggcgccggcgccggcgccggcgccgga 840
Db 781 TCCACTCCCGCAGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGA 840
Qy 841 gaggcagctggggcggtcgcgagctcaagctcagctcagctcagctcagctcagctc 900
Db 841 GAGCGAGCTCGGGCGCGGTGCGCGCGAGCTCAAGCAGTTCTTGGGTGGCTCAAGAG 900
Qy 901 cagcgctactctcaacactcagcttcgctctcagcaccagtgagcgagctgagcgag 960
Db 901 CAGCGTACTCTCAACTCAGCTTCGCTCTACGACAGTGGCGGAGCTGTGATGACG 960
Qy 961 aagtcgacaaagaccgcaacagcacagagcgaggggagtcctgcccctggcgagaggg 1020
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Qy 1021 gcaaggcagaggtctgccaagataagctgtagggtcagggccaccctcctgccaagt 1080
Db 1021 GCACGGCGAGAGGTCTGCCAGATAAGCTGTAGGGGCTCAGGGCCACCTCTCCCTGCCAGT 1080
Qy 1081 ggagcgcagagcgccgaacccaaactggggccacctctgtacctcacttcaggggcact 1140
Db 1081 GGAGACGACGAGCGCCGACCCAACTGGGGCCACCTCTGTACCTTCATCTTTCAGGGC 1140
Qy 1141 gaggccctcagcagagctgggtggcccttgagtcctcaagcgccataaacagctctgact 1200
Db 1141 GAGCCCTCAGCAGGAGCTGGGGTGGCCCTGAGCTCCAGCGCCATAAACAGCTCTGACT 1200
Qy 1201 cccagtgaggccactttgggtgaccccgagtggtgtgtgtgtgtgtgtgtgtgtgtgt 1260
Db 1201 CCCAGCTGAGGCGACCTTTGGGTGACCCCGAGTGGGTGTGTGTGTGTGTGTGTGTGTGT 1260
Qy 1261 ttgagttgctagacccctgcagggctgggggtgagaaaggagtgagcttactcctccat 1320
Db 1261 TTGAGTTGCTAGACCCCTGCCAGGCTGGGGGTGAGAGGGGAGTCACTTCTCCCAT 1320
Qy 1321 tacctagggccctccaaagagtccttttaataaatagctatttaggtgcaaaaaa 1380
Db 1321 TACCTAGGGCCCTCCAAAGAGTCTCTTTAAATAATAGAGCTATTTAGGTGCAAAAAA 1380
Qy 1381 aaaaaa 1391
|||||

Db 1381 AAAAAAAAAA 1391

RESULT 2

V70895

ID V70895 standard; cDNA; 1813 BP.

AC V70895;

DT 17-MAR-1999 (first entry)

DE cDNA encoding an allelic variant of human Zcytor5.

KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;

KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;

KW cardiac pathology; heart enlargement; Zcytor5 ligand; allelic variant;

KW ss. Homo sapiens.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 88..1365

FT /tag= a

FT /product= Zcytor5

PN W09849307-A1.

PD 05-NOV-1998.

PF 01-MAY-1998; 008865.

PR 13-FEB-1998; US-074721.

PR 01-MAY-1997; US-045287.

PR 01-MAY-1997; US-850030.

PR 13-FEB-1998; US-023890.

PA (ZIMO) ZIMOGENERICS INC.

PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,

PI Lok S, Presnell SR, Whitmore TE;

DR WPI; 99-034662/03.

DR P-PSDB: W70861.

PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.

PT down-regulating Zcytor5 natural ligands or detecting cardiostrophin-1

PT in blood

PS Disclosure; Page 68-70; 55pp; English.

CC The present sequence encodes an allelic variant of protein designated

CC Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be

CC administered to down-regulate the effects of a growth and/or maintenance

CC factor in thyroid, heart, and skeletal muscle for example to lessen the

CC effect of cardiostrophin-1 on cardiac pathologies, so preventing heart

CC enlargement. Zcytor5 could be used to detect cardiostrophin-1 in the

CC blood, and to discover other possible Zcytor5 ligands. A probe

CC comprising Zcytor5 DNA or RNA can be used to determine the presence

CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the

CC anti-idiotypic antibody could be used to purify Zcytor5 and

CC therapeutically to modify Zcytor5 ligand effects.

CC Sequence 1813 BP; 415 A; 604 C; 519 G; 275 T;

Query Match

99.08; Score 1377.4; DB 1; Length 1813;

Best Local Similarity 99.88; Pred. No. 5.2e-281;

Matches 1390; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy 1 accctaacggcgccctgccccctgagctctccgtatctcaagctccaccttg 60
Db 313 ACCCTCAATGGCGCCCGCCCGCCCTGAGCTCTCCCGTGTACTCAACGCCCTCACCTTG 372
Qy 61 gctctgccccggccaaacctcaatgggtccaggcagcggtcgggggagacacctgtg 120
Db 373 GCTCTGCCCCGCGCAACCTCAATGGGTCCAGGCAGCGGTGCGGGGGAACACTCGTGTG 432
Qy 121 cagcccgctgacggcagcactcctggctgctctctctctctctctctctctctctct 180
Db 433 CACCGCGGTGACGGCAGCAGCTCTGGCTGGCTCTCTATGTGTGGCTGCGCCCGCAGAG 492
Qy 181 aaacccctcaacatcagctgctggtccaaagaatgagactgagactgagctccgctgacg 240
Db 493 AAACCCGTCAACATCAGCTGCTGGTCCCAAGAACATGAGGACTTGACTGCGCGTGACG 552
Qy 241 ccagggggccacgggggagacctctctccacacacactactccctcaagtagcaagcttag 300
Db 553 CCAGGGGCCCCACGGGAGACCTTCTCTCCACACCACTACTCCCTCAAGTACAGCTTAGG 612
Qy 301 tggtagggcagggaacaacatgtgaggagtacacacagtgggggccccactcctgcac 360

Human granulocyte
Comamonas sp. N-Ac

ALIGNMENTS

RESULT . 1
V27144

V27144;
29-SEP-1998 (first entry)
Nucleotide sequence of clone HFK-66 encoding human NR6
Haemophilin receptor, cell surface protein, cell surface

cell survival; therapeutic; neuronal proliferation; drug screening; ss;

Homo sapiens.

Key	Location/Qualifiers
CDS	1. .1053
	/*tag= a
	/product= "Human NR6"

Product	Product = "Human NR6"
WO9811225-A2.	
19-MAR-1998.	
11-SEP-1997.	
202470	

-002246.

[illegible]

Query Match 16.1%; Score 223.6; DB 1; Length 259;
Best Local Similarity 92.28; Pred. No. 9.1e-39;

Db 8724 CAGATCCGCTACCGCTGGAGGACACGCTGGACTGGAAGTGCCTCCGCCCGGACC 8783
QY 626 -----agtggtggacgatg 640
Db 8784 CGCCCTGACCCCGCCCGGATCTGACTCTCTCCCTACCGTGCAGGTGGTGATGACG 8843
QY 641 tgagcaaccagacctctccgctggcggcctgaaacccggcaccgtgtacttcgtgc 700
Db 8844 TCAGCAACAGACCTCTCTCCGCTCTCGCGGCTGAAGCCCGACCGCTTACTTCGTCC 8903
QY 701 aagtcgctgcaaaccttctgcatctatgctccaaagaacccggagatctggagtgc 760
Db 8904 AAGTGGCTGTACCACTTCGGGATCTATGGTCTGAAGAAGCGGGAATCTGGAGCGAGT 8963
QY 761 ggaagcaccacagcgcctccactcccgccagtg 796
Db 8964 GGAGCCACCCCGCTGCTCCACCCCTCGAAGTG 8999

RESULT 15

V27145
ID V27145 standard; DNA: 6663 BP.
AC V27145;
DT 02-OCT-1998 (first entry)
DE Nucleotide sequence of Murine NR6.
KW Haemopoietin receptor; cell proliferation; cell differentiation;
KW cancer; cell survival; therapeutic; neuronal proliferation; drug;
KW screening; ss; Mouse.
OS Mus sp.
FH Key Location/Qualifiers
FT Key 1182..1744
FT CDS /*tag= a
FT /product= "Murine NR6"
FT /note= "No start or stop codon given"
FN WO9811225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIE/) DZIEGLEWSKA H E.
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willison T,
PI Zhang J;
PI WPI: 98-260970/23.
DR P-PSDB: W55016.
DR New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PS Claim 8; Page 108-114; 182pp; English.
CC The NR6 gene encodes a novel Haemopoietin receptor (HR). Interaction
CC between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and it's
CC products can be used for modulating the activity of the receptors e.g. to
CC regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SQ Sequence 6663 BP; 1462 A; 1852 C; 1715 G; 1634 T;

Query Match 13.7%; Score 190.8; DB 1; Length 6663;
Best Local Similarity 73.5%; Pred. No. 1.2e-31;
Matches 291; Conservative 0; Mismatches 37; Indels 68; Gaps 1;
QY 469 gtgaccacgaccccccgcagctgcagtcgagccgcgtcggggctggagaccag 528
Db 3434 GTGACCACGACCCCGCCCGGATCTGACTCTCTCCCTACCGTGCAGGTGGTGATGACG 3493
QY 529 ctgagctgctgctggtgtgcaccctccctcaaggatttcctcttcaagccaaatc 588
Db 3494 CTGAGTGTGGGTGCTCACCACCGTCTCAAGGATTTCTCTCTTCCAGCCCAAGTAC 3553

QY 589 cagatccgctaccgagtgaggagacagtgtagactgga----- 626
Db 3554 CAGATCCGCTACCGCTGGAGGACACGCTGGACTGGAAGTGCCTCCGCCCGGACC 3613
QY 626 -----agtggtggacgatg 640
Db 3614 CGCCCTGACCCCGCCCGGATCTGACTCTCTCCCTACCGTGCAGGTGGTGATGACG 3673
QY 641 tgagcaaccagacctctccgctggcggcctgaaacccggcaccgtgtacttcgtgc 700
Db 3674 TCAGCAACAGACCTCTCTCCGCTCTCGCGGCTGAAGCCCGACCGCTTACTTCGTCC 3733
QY 701 aagtcgctgcaaaccttctgcatctatgctccaaagaacccggagatctggagtgc 760
Db 3734 AAGTGGCTGTACCACTTCGGGATCTATGGTCTGAAGAAGCGGGAATCTGGAGCGAGT 3793
QY 761 ggaagcaccacagcgcctccactcccgccagtg 796
Db 3794 GGAGCCACCCCGCTGCTCCACCCCTCGAAGTG 3829

Search completed: September 28, 1999, 16:46:31
Job time: 7376 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 28, 1999, 16:40:33 ; Search time 152.56 Seconds
(without alignments)
835.882 Million cell updates/sec

Title: US-09-037-657-24

Perfect score: 1391

Sequence: 1 accctcaaggcgccgcct.....gcaaaaaaaaaaaaaaaaaa 1391

Scoring table: IDENTITY_NUC

Searched: 176461 seqs, 45838279 residues

Database : Issued_Patents_NA.*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/5C_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/5D_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42.6	3.1	4524	4	US-08-845-998-7
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3	40.2	2.9	4403	4	US-08-284-941-1
4	40.2	2.9	4403	5	PCT-US93-02147A-1
5	38.8	2.8	2943	1	US-07-923-976-3
6	38.8	2.8	2855	1	US-07-923-976-5
7	38.8	2.8	3024	1	US-07-923-976-7
8	38.4	2.8	3435	2	US-08-366-577-1
9	38.4	2.8	1055	4	US-08-828-242-2
10	38.4	2.8	3435	5	PCT-US96-00005-1
11	38.2	2.7	9515	3	US-08-812-13
12	38.2	2.7	2752	3	US-08-430-925A-3
13	38.2	2.7	9515	3	US-08-920-827-13
14	38.2	2.7	9515	3	US-08-921-177-13
15	38.2	2.7	9515	3	US-08-362-577C-13
16	38.2	2.7	9515	4	US-08-920-828-13
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21	37.4	2.7	1771	4	US-08-533-669A-7
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23	37.2	2.7	1618	4	US-08-607-509-1
24	37.2	2.7	1618	4	US-08-454-036-1
25	37.2	2.7	1618	4	US-08-634-642-1
26	37.2	2.7	1618	5	PCT-US95-05064-1
27	37	2.7	936	2	US-08-018-977C-4
28	37	2.7	3382	4	US-08-682-847-1
29	37	2.7	1701	5	PCT-US95-16542-1
30	37	2.7	1701	5	PCT-US96-10521-1
31	36.8	2.6	2126	4	US-08-789-354-1
32	36.6	2.6	15664	1	US-08-402-282-3
33	36.6	2.6	15664	1	US-08-508-004-3
34	36.6	2.6	15664	1	US-08-402-066-3
35	36.6	2.6	15664	1	US-08-402-068-3
36	36.4	2.6	28958	1	US-08-258-261B-6
37	36.4	2.6	478	2	US-08-318-193-85

38 36.4 2.6 28958 2 US-08-456-837-6 Sequence 6, Appl1
39 36.4 2.6 28958 2 US-08-457-342-6 Sequence 6, Appl1
40 36.4 2.6 28958 2 US-08-457-646A-6 Sequence 6, Appl1
41 36.4 2.6 28958 2 US-08-458-076A-6 Sequence 6, Appl1
42 36.4 2.6 49377 2 US-08-764-233A-1 Sequence 1, Appl1
43 36.4 2.6 28958 2 US-08-764-233A-4 Sequence 4, Appl1
44 36.4 2.6 28958 2 US-08-457-335A-6 Sequence 6, Appl1
45 36.4 2.6 28958 3 US-08-729-214-6 Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-08-845-998-7
; Sequence 7, Application US/08845998
; Patent No. 5879892
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Coulie, Pierre G.
; APPLICANT: De Smet, Charles
; APPLICANT: Lucas, Sophie
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,998
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)720-3500
; TELEFAX: (617)720-2441
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4524 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 174..1433
US-08-845-998-7

Query Match 3.1%; Score 42.6; DB 4; Length 4524;
Best Local Similarity 47.3%; Pred. No. 0.16;
Matches 129; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

Qy 634 gacgatgtgagcaaccagaccttcgcgcgcctggccgcctggaacccggcaccgtgtac 693
Db 513 GCGGATCTGCTGGACCATCTCTCGCGCTCGGCTCATGGCGCGCGCGCGGC 572
Qy 694 ttcgtgcaagtcgctgcaacccctttggctctatgtctccaaagaaagccggatctgg 753

RESULT 7
US-07-923-976-7

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RESULT 9
US-08-828-242-2
; Sequence 2, Application US/08828242
; Patent No. 5871970
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN

```

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US96/00005
FILING DATE: 2-JAN-96
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.53505
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BMB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3435 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 43..3364
PCT-US96-00005-1

Query Match 2.8%; Score 38.4; DB 5; Length 3435;
Best Local Similarity 51.1%; Pred. No. 1.4;
Matches 90; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 608 aggcagtggtgactgaagtggtgacgatgtgacaaacacagacacctctgcgcctgg 667
Db 2504 ACAGCCGATGGATGCAAGGGGCTGGAGCCGTGCGCAGGACAACTGCCCTCTGTGG 2563
QY 668 ccgctcgaacccgacccgtgactctgtgcaagtgctgcaaccccttggcatct 727
Db 2564 CCACCTGGTCACCTGCTCCTGCTGCGCCGCTGCTCATCGACCGAGACCTGAGGGCGG 2623
QY 728 atggctcgaagaaacccgggatctggagtgtgagtgagccacccacagccgctcc 783
Db 2624 TGGCTCAGCAGGAGGTGATCTCGGACCTGCTGTGCAACCGCATCGATATCTCC 2679
RESULT 11
US-08-920-812-13
; Sequence 13, Application US/08920812
; Patent No. 5763188
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsuhisa, Akio.
; APPLICANT: Uehara, Hirotsugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60608-6402
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/920.812
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362.577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9515 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Pseudomonas aeruginosa,
; STRAIN: Clinical Isolate P2-2
US-08-920-812-13
Query Match 2.7%; Score 38.2; DB 3; Length 9515;
Best Local Similarity 46.4%; Pred. No. 2.2;
Matches 124; Conservative 0; Mismatches 143; Indels 0; Gaps 0;
QY 766 caccacacagccgctcctcactcccccagtgagcccccggggggggggggggggcg 825
Db 6176 CAGCGAGCTCTTCCAAACACCCCTGCAGATACCCGACAGCCCTCGGTATCCAGCGCTGC 6235
QY 826 gaaccgcggcgagagccgagctcgccggcggtgcgcgagctcaagcagttcctg 885
Db 6236 ACCGGAAGCGCGCGCCGCCCTCCAGCCGCGAGAGCCGCCAGCCGCTGTGATGGTG 6295
QY 886 ggctgctcaagaagcagcgctactctcctcaacactcagcttcctccttacgaccagtg 945
Db 6296 GTCGCGAGCCCGCGGAGGATGAGTCGAGCAGCGCAACTGCCGTAGAACAGCGCG 6355
QY 946 cgaagcctgagtcgaagtcgacaaagacccgcaacacagcagggggggtatcctgc 1005
Db 6356 CGGGCCTTCTCCAGGTGCGCGTGCAGACCCGCTGTAGAGCTGGCCGTTAGCGTCGGG 6415
QY 1006 cctcggcgagggcgagcgagag 1032
Db 6416 ATCAGGTTGCGCGCGCGCTGCACCAG 6442
RESULT 12
US-08-430-925A-3
; Sequence 3, Application US/08430925A
; Patent No. 5763252
; GENERAL INFORMATION:
; APPLICANT: Skadsen, Ronald W
; APPLICANT: Tibbot, Brian K
; TITLE OF INVENTION: Cloned Alpha-Glucosidase from Barley
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/430,925A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seay, Nicholas J
 ; REGISTRATION NUMBER: 27,386
 ; REFERENCE/DOCKET NUMBER: 960296.93171
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 608-251-5000
 ; TELEFAX: 608-251-9166
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2752 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 42..2675
 ; US-08-430-925A-3

Query Match 2.7%; Score 38.2; DB 3; Length 2752;
 Best Local Similarity 45.5%; Pred. No. 1.5;
 Matches 179; Conservative 0; Mismatches 208; Indels 6; Gaps 1;
 QY 491 acgtgacgtgagccgctggtgggctgagggaccagctgagcgctgctggtgtgcgc 550
 DB 1501 ACAGAGGACACACCTTTCGGCTCTTCGAGGCCCGCCACGCGGGCGGGTGTGA 1560
 QY 551 caccgcctcgaaggattctcttcttcaagccaaataaccagatccgtaccagatggagg 610
 DB 1561 GGGACACCGCGCGCCCTTCGTGCTCAGCAGGTCCACCTTCGTGGGCTCGGGGGCT 1620
 QY 611 acagtgtgactgaagtggtggagcagtg-----tgagcaaccagacacctctgcgc 664
 DB 1621 ACACCGCTTACTGGAGTGGCGGACCAACCGCCGACCTGGGGCGACCTCGCTACTCCATCA 1680
 QY 665 tggcggcctgaaacccgacccgacccgtgactctgtaagtgcactgcaaccccttggca 724
 DB 1681 ACACCATGCTACGCTTCGGCTCTTCGGCATGCCCATGATCGGCGCGGATCTGCGGGT 1740
 QY 725 tctatggctccaagaagccgggagctctggagtgagtgagagccacacacagccgctcca 784
 DB 1741 TCAACGGCAACACGACAGAGAGAGCTCTGCGGTGGTGGATCCAGCTCGGAGCTTCTACC 1800
 QY 785 ctcccgcagtgagccgcccggccggcgccggcggtgctgcaacccgcgggcgagagc 844
 DB 1801 CPTCTCGAGGGACCACTCGCGCATCTTCACCGTCGCGCGGAGAGTGTACTCTGGCGGT 1860
 QY 845 cgagctggggcgccgtgcgcgcgagctcaagc 877
 DB 1861 CGGTGCGGCGTTCGGCAGGAAGCGCTCGGGC 1893

RESULT 13
 US-08-920-827-13
 ; Sequence 13, Application US/08920827
 ; Patent No. 5770375
 ; GENERAL INFORMATION:
 ; APPLICANT: Ohno, Tsuneya
 ; APPLICANT: Matsuhisa, Akio
 ; APPLICANT: Uehara, Hirotugu
 ; APPLICANT: Eda, Soji
 ; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
 ; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/920,827
 ; FILING DATE: 29-AUG-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/362,577
 ; FILING DATE: 27-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rin-Laures, Li-Hsien
 ; REGISTRATION NUMBER: 33,547
 ; REFERENCE/DOCKET NUMBER: 19036/32420
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/474-6300
 ; TELEFAX: 312/474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9515 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Genomic DNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: Pseudomonas aeruginosa
 ; STRAIN: Clinical Isolate P2-2
 ; US-08-920-827-13

Query Match 2.7%; Score 38.2; DB 3; Length 9515;
 Best Local Similarity 46.4%; Pred. No. 2.2;
 Matches 124; Conservative 0; Mismatches 143; Indels 0; Gaps 0;
 QY 766 caccacacgcccctccactcccgcagtcgagcccgccggcgccggcgccggtgc 825
 DB 6176 CAGCGAGCTCTTCCAAACAACCCCTGCAGATACCGACGCCCTCGGTATCCAGCGCTGC 6235
 QY 826 gaaccgcgggcgagagcgagcgtcgggcggtgctggcgagctcaagcagttccctg 885
 DB 6236 ACCGGAAGCGCGGCGCCGCCACCTCCAGCGGAGAGCCCGCCGCTTGATGGTG 6295
 QY 886 ggctggctcaagaagcacgcgtactgtctcaacctcagcttcgcctctacacacagtg 945
 DB 6296 GTCGGCAGCCCGCGGAGAGTGAAGTCGAGCAGCGGCACTGCCGGTAGAACACGCGG 6355
 QY 946 cgagcctggatgcagaagtcgcacaagaccgcaacacagcacagcaggggagttcttc 1005
 DB 6356 CGGGCCTTCTCCAGGTGCGCGTCGAGCAGCCGCTGTGTAGAGCTGGCCGTTGAGCTCGG 6415
 QY 1006 cctcgggcagacggggcgagcgagag 1032
 DB 6416 ATCAGGTTCCGCGCGCGCTGCACCAG 6442

RESULT 14
 US-08-921-177-13
 ; Sequence 13, Application US/08921177
 ; Patent No. 5798211
 ; GENERAL INFORMATION:
 ; APPLICANT: Ohno, Tsuneya
 ; APPLICANT: Matsuhisa, Akio
 ; APPLICANT: Uehara, Hirotugu

APPLICANT: Eda, Soji
 TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/921,177
 FILING DATE: 29-AUG-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/362,577
 FILING DATE: 27-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Rin-Laures, Li-Hsien
 REGISTRATION NUMBER: 33,547
 REFERENCE/DOCKET NUMBER: 19036/32420
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9515 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 ORIGINAL SOURCE:
 ORGANISM: Pseudomonas aeruginosa
 STRAIN: Clinical isolate P2-2
 PS-08-921-177-13

Query Match	2.7%;	Score 38.2;	DB 3;	Length 9515;
Best Local Similarity	46.4%;	Pred. No. 2.2;		
Matches 124;	Conservative 0;	Mismatches 143;	Indels 0;	Gaps 0;

QY	766	caccacacagcgcgcctccactcccccgaagtgaagcccccggcccgccggcgccggggcggtgc	825
Db	6176	CAGCGCAGCTCTTCCAACAACCCCTGCAGATACCGACAGGCCCTCGGTATCCAGCGCCTGC	6235
QY	826	gaaccgccccggcgagacgcagctccggggccggtgctggcgcgagctcaagcagttctcgtg	885
Db	6236	ACCGGAAGCGCGCGCGCCCCACCTCCAGGCCGAGAGAGGCCAGCGCGGCTTGATGGTG	6295
QY	886	ggctggctcaagaacgcgcgtactgctccaacctcagcttcgcgcctcttcagcaccagtgg	945
Db	6246	GTCCGCAGCCCGCGCGGAGAGTGAAGTCGAGACGCCGCAACTCCCGGTAGACAGCGCG	6355
QY	946	cgagctggatgcagaagctgcacaagaaccgcgaaccagcacagcagggggtactctgc	1005
Db	6356	CGGGCCTTCTCCAGTGC CGCTCGAGCACCGCGCTGGTAGACTGGCGCTTGACGCTGGG	6415
QY	1006	cctcgggcagagaggggcacggcgagag	1032
Db	6416	ATCAGETTCGGCGCGCGCTGCACGAG	6442

RESULT 15
US-08-362-577C-13
; Sequence 13, Application US/08363577C
; Patent No. 5807673
; GENERAL INFORMATION:

APPLICANT: Ohno, Tsuneya
 APPLICANT: Matsuhisa, Akio
 APPLICANT: Uehara, Hirotsugu
 APPLICANT: Eda, Soji
 TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/362,577C
 FILING DATE: 27-MAR-1995
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Rin-laures, Li-Hsien
 REGISTRATION NUMBER: 33,547
 REFERENCE/DOCKET NUMBER: 19036/32420
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9515 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 ORIGINAL SOURCE:
 ORGANISM: Pseudomonas aeruginosa
 STRAIN: Clinical isolate P2-2
 US-08-362-577C-13

Query Match	2.78;	Score 38.2;	DB 3;	Length 9515;
Best Local Similarity	46.4%;	Pred. No. 2.2;		
Matches 124;	Conservative 0;	Mismatches 143;	Indels 0;	Gaps 0;

Qy	766	cacccacagcgcctccactcccgcagtcgagcgccggccccggcgcgggcggtgc 825
Db	6176	CAGCGCAGCTCTTCCAAACAACCCCTGTCAGATACCAGACAGCCCTCCGTATCCAGCGCCCTGC 6235
Qy	826	gaaccgcggggcgagagcgcagtcgcggggcggtgcggcgcgagtcaagcagttctctg 885
Db	6236	ACCGAAGGGCGGGGCCGCCCACTCCAGGCGCGGAGAGCCCGAGCGGCCCTTGATGGTG 6295
Qy	886	ggcttggctccaagaagcacgcgtactgtctccaaacctcagcttcgcctcttacgccagtgg 945
Db	6296	GTCGCAGGCCCGCGCGGAGGATGAAGTCGAGCAGCGGCAACTGCCGGTAGAACACAGCGCG 6355
Qy	946	cgagccttgatgcagaagtctgcacaagaaccgcgcaaccgcagcacagaggggatcctgc 1005
Db	6356	CGGGCCTCTTCAGAGTCGCCGCTCGAGCACCGCCTGGTAGCTGGCCGTTGACGCTCGGG 6415
Qy	1006	cctcgggcagagcggggcaggcgagag 1032
Db	6416	ATCAGGTTCCGGCGCGCGCTGCACCAAC 6442

Search completed: September 28, 1999, 16:40:56
Job time: 7042 sec

Query Match	22.5%	Score 313.2	DB 42	Length 364
Best Local Similarity	94.5%	Pred. No. 4.6e-56		
Matches 346	Conservative 0	Mismatches 18	Indels 2	Gaps 2
QY 1013	cagacggggcagcgacagaggtcctgcagataagctgtaggggctcaggccacccctccc	1072		
Dbb				
364	CAGACGGGGCACGGCAGAGGTCCTGCACAGATAAGCTGTA-GGGCTCAGGCACGCCCTCCC	306		
QY 1073	tgcacagtggagcgcagagcgcaaacccaaactggggccacctctgtaccctcacctca	1132		
Dbb				
305	TGCCACGTGGAGACGCAGAGCGCAACCCAAACTGGGGCCACCTCTGTACCTCAGCTCA	246		
QY 1133	gggcacctgaagccctcagcaggagctggggtggccctgagctccaacggccataacag	1192		
Dbb				
245	GGGCACCTGGACACCTCTACAGAGAGCTGGGTGGCCCTGAGCTCCAAGGCCATAACAG	186		
QY 1193	ctctgactccacagtgaggccacctttgggtgcaccccaagtgggtgtgtgtgtgtgtg	1252		
Dbb				
185	CTCTGACTCCACAGTGAGCCACCTTTGGGTGCA-CCCATGGGTGTGTGTGTGTGTGTG	127		
QY 1253	agggttggttgagttgcctagaacccctgcagggctgggggtgagaagggagctcata	1312		
Dbb				
126	AGGGTTGGTGTGAGTTGCCTAGAACACCTGCCAGGGCTGGGGGTGAGGAGGGAGTCATA	67		
QY 1313	ctccccattacctaggccccctccaaaagagtccttttaataaataagctatttaggtg	1372		
Dbb				
66	CTCCCATACCTAGGGGCCCTCCAAAAGAGTCCTTTAAATAAATGAGCTATTTAGGTG	7		
QY 1373	caaaaa 1378			
Dbb				
6	CAAAA 1			

[illegible]

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Dec 30, 1996 this sequence version replaced gi:1528951.

Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:289787
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 437.

FEATURES
Source
1. 464
Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:479043"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand CDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACCAATCTCAAGTGGAGCGCGGAAATTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 1]; double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 102 a 144 c 130 g 88 t
ORIGIN

Query Match 27.4%; Score 380.8; DB 29; Length 464;
Best Local Similarity 88.8%; Pred. No. 4e-70; Mismatches 0; Gaps 0;
Matches 412; Conservative 0; Indels 52; Indels 0; Gaps 0;
QY 197 gctgtgttccaaagacatgaaggacttgacctgcgctggagccagggccacgggg 256
Db 1. GCTGTGTGTCGGGACATGAAGATCTCACGTGCGGTGGACCGGTGACCGGG 60
QY 257 agacctctccacacccaactactcctcaagtcacaaagcttgggtggtatggccaggaca 316
Db 61 AGACATCTTACATACCACTACTCCCTCAAGTACAAAGCTGAGGTGATACGTCAGGATA 120
QY 317 acacatgtgagagtagcacacacagtgggggccactctgccaactcccaaggacctgg 376
Db 121 ACACATGTGAGGAGTACACACTGTGGGCGCTCATCTATGCCATATCCCAAGGACCTGG 180
QY 377 ctctctttacgcccctatgagatctgggtgggggcccacacacgctgggctgcccct 436
Db 181 CCCTCTTCACTCCCTATGAGATCTGGTGGAGGCCACCAATCGCTAGCTCAGCAAT 240
QY 437 ccgagtactacgtgatatctctggtatgtggtgaccacggaccccccccgacgtgc 496
Db 241 CTGATGCTTACACTGTGATCTCTGGACGTGGTGACACACGACCCCCACCCGAGGTGC 300
QY 497 acgtgagcgcgtcgggggcctggagggaccagctgagcgtgcgtgggtgtgcgaccgcg 556
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Db 301 ACGTGAGCGCGGTTGGGGGCTTGAGGACCAAGCTGAGTGGCGTGTCCACCACAG 360
QY 557 ccctcaagattctctctttcaagccaataaccagatccgctaccgagtgagagcagtg 616
Db 361 CTCCAAGGATTTCTCTTCCAGCCCAAGTACCAAGATCCGCTACCGCGTGAGGACAGCG 420
QY 617 tggactgaaagtggtgagcagatgagcaacacagacctctctgc 660
Db 421 TGGACTGGAAGTGTGTGATGACGTGAGCAACCAAGACCTCTCTGC 464

RESULT 5
AI264328/c 398 bp mRNA EST 27-JAN-1999
LOCUS
DEFINITION
3', mRNA sequence.
ACCESSION
AI264328
NID
93872531
VERSION
AI264328.1 GI:3872531
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 398)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
On Jan 14, 1998 this sequence version replaced gi:1797852.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1350
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 699 Std Error: 0.00
Seq primer: 40UP from Gibco
High quality sequence stop: 397.
Location/Qualifiers
1. 398
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1855976"
/clone_lib="Soares-NHMPu-S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: p7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT 74 a 123 c 117 g 84 t
ORIGIN

Query Match 27.4%; Score 380.8; DB 44; Length 398;
Best Local Similarity 99.0%; Pred. No. 3.9e-70;
Matches 394; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
QY 979 aacagacacagagagggatcctgcctgggagacagggcgagaggtctctg 1038
Db 398 AACACACAGGACGAGGGATCTGCTCCCTCGGACAGCGGCGGACGAGGTCTTG 339
QY 1039 ccagataagctgtgagggctcagggcaccctcctgcacgtggagacgagggccgaa 1098
|||||

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BASE COUNT      77 a   134 c   129 g   91 t
ORIGIN

Query Match      29.2%; Score 406.4; DB 28; Length 431;
Best Local Similarity 99.3%; Pred. No. 1.8e-75;
Matches 429; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 943 tgccgagcctggatgcagaaagtgcacacagaccacacacacagcaggcggtac 1002
Db 431 TGCGAGCCTGGATGCAGAAGTCGACAAAGCCGCCAAGACCACAGCACAGGAGGGATCC 372
QY 1003 tgccctcgagcacacggggcagcgagagtgcttcctccagataaagctgttaggggctcagg 1062
Db 371 T-CCCTCGGCGACACGGGGCAGCGCGAGAGGTCTTCCAGATAAAGCTGTAGGGGCTCAGG 313
QY 1063 ccaccttcccctgcacgtggagacgagagggccgaacccaacactggggccacctctgttac 1122
Db 312 CCACCTCCCTGCACGTGGAGACGACGAGGCGCGAACCAACTGGGGGCCACCTCTGTAC 253
QY 1123 cctcaattcaggcactgagc--cctcagcagagagctggggggccccctgagctccaac 1181
Db 252 CCTCACTTCAGGCGACCTGACCACTCCCTCAGCAGAGGTGGGGTGCCCCCTGAGCTCCAAC 193
QY 1182 ggccataaacgctgactcccacgtgagggcaccctttgggtgcacccccagtggtgtgt 1241
Db 192 GGCCATAAACAGCTCTGACTCCCACGTGAGGCCACCTTTGGGTGCACCCCACTGGGTGTGT 133
QY 1242 gtgtgtgtgaggggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1301
Db 132 GTGTGTGTGTGAGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 73
QY 1302 gggagtcattactccccattacttagggccccctccaaaagagctcttttaataaatag 1361
Db 72 GGGAGTCATTACTCCCATTAACCTTAGGGCCCCCTCCAAAAGAGTCTTTTAATAAATGAG 13

QY 1362 ctattaggtgc 1373
Db 12 CTATTAGGTGC 1

RESULT 3
AA922128/c 469 bp mRNA EST 23-JUN-1998
LOCUS om45el2.s1 Soares_NFL_T_GBC_S1 Homo sapiens CDNA clone
DEFINITION IMAGE:1544014.3, mRNA sequence.
ACCESSION AA922128
NID g3069437
VERSION AA922128.1 GI:3069437
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 469)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On May 8, 1995 this sequence version replaced gi:800381.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 763 Std Error: 0.00
Seq primer: -40m3 fwd. Et from Amersham
High quality sequence stop: 448.
Location/Qualifiers
1. .469
/organism="Homo sapiens"
/db_xref="taxon:9606"

FEATURES
source
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KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Carnivora; Homnidae; Homo.

AUTHORS 1 (bases 1 to 457)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chisoso, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.
and Marini, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 9704478

COMMENT On Sep 12, 1996 this sequence version replaced gi:1393691.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is 468
Insert Length: 542 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham.

Location/Qualifiers
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/clone="IMAGE:490004"
/clone_lib="Soares_pregnant_uterus_NbHpu"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: uterus; Vector: p7T73-Pac; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
AATGGAGAAATCGCGCGCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7T73 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

BASE COUNT 96 a 144 c 139 g 84 t 4 others

ORIGIN

Query Match. 30.6%; Score 425.4; DB 29; Length 467;
Best Local Similarity 98.3%; Pred. No. 2,1e-79;
Matches 460; Conservative 0; Mismatches 4; Indels 4; Gaps 3;

QY 909 ctgctccaacctcagcttcgcctctacaccagtcgagcctggaatgcagaagtgcga 968
Db 1 CTGCTCAACCTCAGCTTCGGCTCTACGACACAGTGGCGAGCTGGATGACAGAGTCGCA 60
QY 969 caagaccgcgaaccagcacagcagcaggggagatcctgcctcgggcagacg-gggcacggc 1027
Db 61 CAAGACCCGCAACCAACGACGACGAGGAGGATCCTGCCCTCGGGNNANCGNGGCGACGGC 120
QY 1028 gagaggtcctgcagataagctgtaggggctcaggccacctccctgccacgtggagacg 1087
Db 121 GAGAGTCTCTGCAGATAGCTGTAGGGCTCAGGCGACCTCCCTGCCACGTGGAGACG 180
QY 1088 cagagcgccgaacccaaactggggccacctctatacctcacttcaggcgacctgagc--c 1145
Db 181 CAGAGGCCGAACCCAACTGGGGCCACCTCTGTACCCTCCTTCAGGGCACCTGAGCCAC 240

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 28, 1999, 15:38:17 : Search time 2095.87 seconds

(without alignments)
1309.143 Million cell updates/sec

Title: US-09-037-657-24

Perfect score: 1391
Sequence: 1 accctcaagcgcgccgct.....gcaaaaaaaaaaaaaaaaaa 1391

Scoring table: IDENTITY_NUC

Searched: 2546578 seqs, 986266752 residues

Database :

EST: *
1: em_est1: *
2: em_est2: *
3: em_est3: *
4: em_est4: *
5: em_est5: *
6: em_est6: *
7: em_est7: *
8: em_est8: *
9: em_est9: *
10: em_est10: *
11: em_est11: *
12: em_est12: *
13: em_est13: *
14: em_est14: *
15: em_est15: *
16: em_est16: *
17: em_est17: *
18: em_est18: *
19: em_est19: *
20: em_est20: *
21: em_est21: *
22: em_est22: *
23: em_est23: *
24: em_est24: *
25: em_est25: *
26: em_est26: *
27: em_est27: *
28: em_est28: *
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45: em_est45: *
46: em_est46: *
47: em_est47: *
48: em_est48: *
49: em_est49: *
50: em_est50: *
51: em_est51: *
52: em_est52: *
53: em_est53: *

54: em_est22: *
55: em_est23: *
56: em_est24: *
57: em_est25: *
58: em_est26: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query				ID	Description
	Score	Match	Length	DB		
1	425.4	30.6	467	29	AA127694	AA127694 z89c11.r
2	406.4	29.2	431	28	AA121532	AA121532 z89c11.s
3	394.8	28.4	469	40	AA922128	AA922128 om45e12.s
4	380.8	27.4	464	29	AA049280	AA049280 m145d02.r
5	380.8	27.4	388	44	AI264328	AI264328 q109c05.x
6	373.4	26.8	389	46	AI417616	AI417616 t980c02.x
7	368.4	26.5	482	26	W66776	W66776 mel1b11.r1
8	365.8	26.3	394	40	AA927378	AA927378 om27a08.s
9	359.2	25.8	415	40	AA992638	AA992638 ut-r-A0-a
10	334.4	24.0	428	45	AA866388	AA866388 ut-r-A0-a
11	327.8	23.6	433	33	AA06406	AA06406 z44a09.s
12	326.6	23.5	394	37	AA06010	AA06010 z44a09.s
13	321.4	23.1	356	45	AI375784	AI375784 q259908.x
14	313.2	22.5	364	42	AI085207	AI085207 oy16c04.s
15	307	22.1	477	43	AI185924	AI185924 qe50c05.x
16	305.4	22.0	474	46	AI421423	AI421423 t425h01.x
17	296	21.3	466	43	AI161002	AI161002 qb69g04.x
18	294.4	21.2	466	43	AI185780	AI185780 qe44h04.x
19	293.4	21.2	311	42	AI16720	AI16720 qb94d05.x
20	293.4	21.2	462	45	AI394468	AI394468 t179d12.x
21	283.4	20.3	448	26	W46603	W46603 zc32h10.r1
22	262	18.8	431	25	AI333812	AI333812 qp33e12.x
23	261	18.6	443	26	W37175	W37175 zb21a02.r1
24	259	18.6	447	43	AI187074	AI187074 qe38a03.s
25	250.2	18.0	458	27	AA043001	AA043001 zk36f01.r
26	237.4	17.1	244	45	AI383213	AI383213 tc76c11.x
27	230	16.5	417	44	AI269388	AI269388 q126b05.x
28	228.4	16.4	247	32	AA049278	AA049278 EST90550
29	224.2	16.1	503	29	AA049278	AA049278 m145c04.r
30	193.2	13.9	385	50	AI670108	AI670108 w655f03.x
31	187.8	13.5	470	43	AI233311	AI233311 EST129999
32	183.4	13.2	410	27	AA042914	AA042914 zk56f01.s
33	172.8	12.4	404	42	AI074921	AI074921 oy04d08.s
34	172.6	12.4	464	41	AI074408	AI074408 ut-r-C2-n
35	160.2	11.5	445	27	AA039053	AA039053 m199d07.r
36	151	10.9	218	22	H14009	H14009 EST0035.CH
37	124	8.9	273	23	R87407	R87407 ym88d09.s1
38	122	8.2	390	26	W17583	W17583 mb75d01.r1
39	114.6	8.2	465	26	W46604	W46604 zc32h10.s1
40	106.6	7.7	332	48	AI579568	AI579568 ut-r-GO-u
41	101.4	7.3	227	30	AA270365	AA270365 va63h12.r
42	95.8	6.9	319	48	AI574687	AI574687 ut-r-GO-u
43	67.4	4.8	456	34	AA488477	AA488477 ab37d07.r
44	47.8	3.4	107	27	AA014965	AA014965 mh23e02.r
45	44.8	3.2	316	47	AI464866	AI464866 m292e02.y

ALIGNMENTS

RESULT 1
LOCUS AA127694 467 bp mRNA
DEFINITION z89c11.r Soares pregnant uterus_NbHPU Homo sapiens CDNA clone
IMAGE:480004 5', mRNA sequence.
ACCESSION AA127694
NID 91686983
VERSION AA127694.1 GI:1666983

QY 241 ccaggggcccacgggagaccttcctccacacccaactactccctcaagtacaagcttagg 300
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Db 410 CCAGGGCCCCACGGNGAGACTTCTCCACACCAACTACTCCCTCAAAGTACAAGCTTAGG 469
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QY 301 tggatatgg 308
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Db 470 TGGTATGG 477
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Search completed: September 28, 1999, 15:38:23
Job time: 3291 sec

ORIGIN

Query Match	1.88;	Score 123;	DB 34;	Length 91638;
Best Local Similarity	75.88;	Pred. No. 1.2e-19;		
Matches 150;	Conservative 0;	Mismatches 48;	Indels 0;	Gaps 0;
QY 337	tatttgattttatgaaaaatacacctgtttgatattgtttggtttggtttgagttttgtt	396		
Db 54875	TCATTCCTTGTCTTTACATCTGGTTTGGGTTTTTGGGTTTTTGTGTTTTGTTT	54934		
QY 397	tatttgagacagggctctctctgtgtagtcctctgggtgtctcttggaaactcacctctgtagacc	456		
Db 54935	TTTTTGAGACAGGGTTTCTCTGTAGCCCTGGCTGTCTCTGAANCACATTTGTAGACC	54994		
QY 457	agcttgcccttgaaactcagaaataccgctctgtctgtctcccaagtcgttagataaagg	516		
Db 54995	AGCGTGCCCTCGAACTCAGAAATTCACCTGCTCTGCTCCCAAGTGTGGGATTAAGG	55054		
QY 517	tgtgcaactgcccattcagc	534		
Db 55055	NNTGTGCACCATCTGC	55072		

RESULT 14
 AC003066
 LOCUS
 DEFINITION
 ACCESSION
 NID
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 HTG
 21-MAY-1999
 Mus musculus chromosome 16 clone tbx1, WORKING DRAFT SEQUENCE, S
 179436 bp
 DNA
 Mus musculus chromosome 16 clone tbx1, WORKING DRAFT SEQUENCE, S
 unordered pieces.
 AC003066
 94883622
 AC003066.9 GI:4883622
 HTG; HTGS_PHASE1.
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 179436)
 Zhang, G. and Roe, B.A.
 Mouse Chromosome 16 BAC Clone tbx1
 Unpublished (1997)
 2 (bases 1 to 179436)
 Emanuel, B. and Budarf, M.
 Mouse Chromosome 16 BAC Clone tbx1
 Unpublished (1997)
 3 (bases 1 to 179436)
 Zhang, G., Lao, V., Zhan, M. and Roe, B.A.
 Direct Submission
 Submitted (06-NOV-1997) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA

ON MAY 21, 1999 this sequence version replaced gi.4835801.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 5 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * as soon as it is available and the accession number will
 * be preserved.

FEATURES	source
1	Location/Qualifiers
3130:	contig of 3130 bp in length
3222:	gap of unknown length
3223:	contig of 5059 bp in length
3281:	gap of unknown length
8373:	gap of unknown length
8374:	23378: contig of 15005 bp in length
23379:	23470: gap of unknown length
23471:	88686: contig of 65216 bp in length
89687:	88778: gap of unknown length
89779:	179436:: contig of 90658 bp in length.
1:	179436
/organism="Mus musculus"	
/db_xref="taxon:10090"	

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ORIGIN	/clone="tbx1" /chromosome="16"				

[illegible]

RESULT 15
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 DEFINITION
 ACCESSION
 NID
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 AC003067
 39061 bp
 DNA
 Mus musculus chromosome 16 clone tbx3, WORKING DRAFT SEQUENCE, 7
 unordered pieces.
 AC003067
 g3818367
 AC003067.1 GI:3818367
 HTG; HTGS_PHASE1.
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 39061)
 Zhang, G. and Roe, B.A.
 Mouse Chromosome 16 BAC Clone tbx3
 Unpublished (1997)
 2 (bases 1 to 39061)
 Emanuel, B. and Budarf, M.
 Mouse Chromosome 16 BAC Clone tbx3
 Unpublished (1997)
 3 (bases 1 to 39061)
 Zhang, G., Lao, V., Zhan, M. and Roe, B.A.
 Direct Submission
 Submitted (06-NOV-1997)

DATE	BY	COMMENT
08. 7. 2019	USA	On Oct 31, 1998 this sequence version replaced gi.3132482.
		* NOTE: This is a 'working draft' sequence. It currently
		* consists of 7 contigs. The true order of the pieces
		* is not known and their order in this sequence record is
		* arbitrary, gaps between the contigs are represented as
		* runs of N, but the exact sizes of the gaps are unknown.
		* This record will be updated with the finished sequence.
		* as soon as it is available and the accession number will
		* be preserved.

*	I	2173:	contig	of 2173 bp in length
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*	2244	4741:	contig of 2498 bp in length	
*	4742	4811:	gap of unknown length	
*	4812	7078:	contig of 2267 bp in length	
*	7079	7148:	gap of unknown length	
*	7149	10018:	contig of 2870 bp in length	
*	10019	10088:	gap of unknown length	
*	10089	13065:	contig of 2977 bp in length	
*	13066	13135:	gap of unknown length	


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BASE COUNT 167 a 274 c 225 g 168 t
ORIGIN

Query Match 3.8%; Score 254.4; DB 5; Length 834;
Best Local Similarity 99.6%; Pred. No. 7.9e-52;
Matches 255; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1185 cccaccccttcacggctccctcgaagctaccctgctctatacatagagacacacct 1244
Db 1 CCCACCCCTTCTCATCGGCTCCTCCCTGCAAGCTACCTGCTCTATACATGGAGACACACCT 60

Qy 1245 ggggccacgcgtgggggctctactgacacctcaatggtccgcctcctcctcgtgctg 1304
Db 61 GGGGCCACCGCTGAGGGCTCTATGTGACCTCAATGGTCCGCCCTGCGCTCTGAGCTG 120

Qy 1305 tccgcctccttaacacccctcaccctggcctggcctggcctggccttaatgggtccagg 1364
Db 121 TCCGCGCTCCTTAACACCTCCACCTGGCCCTGGCCCTGCTAACCCTAATGGTCCAGG 180

Qy 1365 cagcagtcagagacaaatctggtgtgacccgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1424
Db 181 CAGCAGTCAGGAGCAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240

Qy 1425 tgcctctatgtgct 1440
Db 241 TGCCTCTATGTGGCT 256

RESULT 9
LOCUS AF059293 1716 bp mRNA PRI 02-AUG-1998
DEFINITION Homo sapiens cytokine-like factor-1 precursor (CLF-1) mRNA,
complete cds.
ACCESSION AF059293
NID 9372626
VERSION AF059293.1 GI:3372626
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1716)
AUTHORS Elson,G.C.A., Graber,P., Losberger,P., Herren,S., Gretener,D.,
Menoud,L.N., Wells,T.N.C., Kosco-Vilbois,M.H. and Gauchat,J.F.
TITLE CLF-1, a Novel Soluble Protein Shares Homology With Members of the
JOURNAL Cytokine Type-I Receptor Family
AUTHORS J. Immunol. (1998) In press
REFERENCE 2 (bases 1 to 1716)
AUTHORS Elson,G.C.A., Graber,P., Losberger,P., Herren,S., Gretener,D.,
Menoud,L.N., Wells,T.N.C., Kosco-Vilbois,M.H. and Gauchat,J.F.
TITLE Direct Submission
JOURNAL Submitted (14-APR-1998) Dept. of Immunology, Sero-Pharmaceutical
Research Institute, 14, Chemin des Aulx, Plan-les-Ouates, GE 1228,
Switzerland
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119..1387
CDS

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similar to the sequence presented in GenBank Accession
Number AC003112"
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GETFLHTNYSLAYKLRTWGDNTCEYHTVGPCHSKIPKDLALTPYETVETATNRLG
SARSDVLLIDVLDVITDPPDPPDPPDPPDPPDPPDPPDPPDPPDPPDPPDPPD
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295 a 623 c 525 g 273 t
BASE COUNT
ORIGIN

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Best Local Similarity 86.5%; Pred. No. 1.9e-43;
Matches 243; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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Db 234 ACACAGCTGTGATCAGTCCCGAGGATCCACAGCTTCTCATCGGCTCCTCCTGCTGCCA 293

Qy 1219 cctgctctatacatgagacacacccctggggccaccgctgaggggctctactgagacctca 1278
Db 294 CCGTCTCAGTGCAGGAGACCCACGAGGACCCACCGCGGAGGCGCTCTACTGGACCTCA 353

Qy 1279 atggtccgcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 1338
Db 354 ACGGGCGCGCGCTGCGCGCTGAGCTCTCCGCTGACTCAACGCGCTCCTCCTGCTCTGG 413

Qy 1339 cctcgttaacacctaatggtccagcagcagcagcagcagcagcagcagcagcagcagc 1398
Db 414 CCTGGCCACCTCAATGGTCCAGGAGGCGGTGCGGGGACACCTCGTGTGCCACGCC 473

Qy 1399 gagacgcagcattcgtggtgctcctcctcctcctcctcctcctcctcctcctcctc 1439
Db 474 GTGACGCGAGCATCCTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 514

RESULT 10
LOCUS AF0394 1391 bp DNA PAT 07-MAY-1999
DEFINITION Sequence 24 from Patent WO9811225.
ACCESSION AF0394
NID 94774672
VERSION AF0394.1 GI:4774672
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1391)
AUTHORS Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Raker,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
TITLE A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
JOURNAL Patent: WO 9811225-A 19-MAR-1998;
NICOLA NICOS ANTONY (AU)
FEATURES
Location/Qualifiers
1..1391
source

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SW:IL6B_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN
PRECURSOR (274..431); 93% identity.---

Query Match 7.3%; Score 484.6; DB 11; Length 40668;
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Matches 1294; Conservative 0; Mismatches 904;

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uterus NBHPU Homo sapiens cDNA clone 490063 5' (1..110);
93% identity. --(10466..10548) DHS similarity to AA452628
zx33f04.rl Soares total fetus NB2HF8 9W Homo sapiens cDNA
clone 788287 5' (1..82); 95% identity. --(10486..10548) DHS
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identity. --DHS similarity to AAL36115 zk90b04.rl Soares
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clone 365523 5' (145..346); 96% identity. --(11121..11331)
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NBH19W Homo sapiens cDNA clone 365523 3' (429..307); 95%
identity. --(11127..11246) DHS similarity to AA047548
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(309..229); 99% identity."
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to W37175 zb21a02.rl Soares fetal lung NBH19W Homo
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99% identity. --(15227..14897) DHS similarity to W46603
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identity. --(15227..15088) DHS similarity to W46604
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fibroblasts NBHSF Homo sapiens cDNA clone 324067 5'
(351..329); 100% identity. --(15735..15713) DHS similarity
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PIR:B38252 B38252 granulocyte colony-stimulating factor
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VERSION	AC003112.1	GI:2636669	
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SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Lamerdin, J.E., McCready, P.M., Adamson, A.W., Burkhardt-Schultz, K., Gordon, L., Christensen, M., Kyle, A., Ramirez, M., Stillwagen, S., Barnes, J., Pangnan, L., Bruce, R., Quan, G., Montgomery, M., Ow, D., Kobayashi, A., Olsen, A.O. and Carrano, A.V.		
TITLE	Sequence analysis of an ~1 Mb region containing the MEF2B gene in 19p12		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 40668)		
AUTHORS	Lamerdin, J.E.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-NOV-1997) Human Genome Center, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA		
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 AUTHORS Nicola,N.A., Fabri,D., Farley,A., Nash,A., Willson,T., Rakar,S., Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and Kikuchi,Y.
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GenCore version 4.5
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OM nucleic : nucleic search, using sw model

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41: em_hum4.*
42: gb_pr4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	6561.6	98.5	11832	5	A70408	A70408 Sequence 38
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4	738.8	11.1	1930	5	A70392	A70392 Sequence 22
5	484.6	7.3	40668	11	AC003112	AC003112 Human DNA
6	280.4	4.2	1629	5	A70382	A70382 Sequence 12
7	280.4	4.2	1673	5	A70384	A70384 Sequence 14
8	254.4	3.8	834	5	A70388	A70388 Sequence 18
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10	190.8	2.9	1391	5	A70394	A70394 Sequence 24
11	141.2	2.1	560	5	A70393	A70393 Sequence 23
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22	116	1.7	1349	12	MUSCYCP4	K03127 Mouse cytoc
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ALIGNMENTS

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DEFINITION					
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NID	94774676				
VERSION	A70398.1	GI:4774676			
KEYWORDS					
SOURCE	unidentified.				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 6663)				
AUTHORS	Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Raker, S., Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and Kikuchi, Y.				
TITLE	A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME				
JOURNAL	Patent: WO 9811225-A 19-MAR-1998;				
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BASE COUNT	1462 a 1852 c 1715 g 1634 t				
ORIGIN					

Search completed: September 28, 1999, 16:46:12
Job time: 7359 sec

Truncated upstream
Upstream region of

ALIGNMENTS

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ALIGNMENTS

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		02-OCT-1998 (first entry)
		Nucleotide sequence of Murine NR6.
		Haemopoietin receptor; cell proliferation; cell differentiation;
		cancer; cell survival; therapeutic; neuronal proliferation; drug
		screening; ss; Mouse.
		Mus sp.

Scoring table: IDENTITY_NUC

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WO9811225-A2.
19-MAR-1999

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PA Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
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PI Zhang J;
DR WPI; 98-260970/23.
DR P-PSDB; W5016.
DR New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PS Claim 8; Page 108-114; 182pp; English.
CC The NR6 gene encodes a novel Haemopoietin receptor (HR). Interaction
CC between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and its
CC products can be used for modulating the activity of the receptors e.g.
CC regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present
CC therapeutically used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis
CC e.g. for cancers or predisposition to cancers, or for drug screening;
SQ sequences 5663 BP; 1462 A; 1852 C; 1715 G; 1634 T;

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Best Local Similarity 100.0%; Pred. No. 0;
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 PD 19-MAR-1998.
 PF 11-SEP-1997; G02479.
 PR 11-SEP-1996; AU-002246.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI (DZIE/) DZIELEWSKA H E.
 PI Alexander W, Fabry L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
 PI Zhang J;
 DR WPI; 98-260970/23.
 PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PT e.g. neuronal cells
 PS Claim 9; Fig 3; 18pp; English.
 CC The NR6 protein is a novel Haemopoietin receptor (HR). Interaction
 CC between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and its
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence. 11832 BP; 2447 A; 3367 C; 3298 G; 2720 T;

Query Match 98.5%; Score 6561.6; DB 1; Length 11832;
 Best Local Similarity 99.6%; Pred. No. 0;
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PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIE/) DZIELEWSKA H E.
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
PI Zhang J;
DR WPI; 98-260970/23.
DR P-PSDB; W55013.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PS Claim 6; Page 90-92; 182pp; English.
CC The haemopoietin receptor (HR) NR6.3 is a form of the novel HR NR6.
CC Interaction between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and it's
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
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PN WO9849307-A1.
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 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 13-FEB-1998; US-850030.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZIMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR P-PSDB; W0860.
 DR P-PSDB; W0860.
 PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
 PT down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Disclosure: Page 63-66; 55pp; English.
 CC The present sequence encodes a protein designated Zcytor5, which is
 CC a cytokinin-like receptor. Soluble Zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible Zcytor5 ligands. A probe
 CC comprising Zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytor5 and
 CC therapeutically to modify Zcytor5 ligand effects.
 SQ Sequence 1690 BP; 319 A; 592 C; 505 G; 274 T;

Query Match 3.3%; Score 221.8; DB 1; Length 1690;
 Best Local Similarity 86.8%; Pred. No. 1.le-48;
 Matches 244; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1159 acacagctgtaatacagcccccagaccacccctctcatggtctccctcgaaagcta 1218
 DB 167 ACACAGCTGTGATCAGTCCCGAGGATCCACGCTTCTCATCGGCTCTCCCTGCGGCA 226
 QY 1219 cctgctctatacatgagacacacccctggccagcctgaggggtctactggacctca 1278
 DB 227 CCTGCTCAGTGCAGCAGACCCACCCAGGAGCCACCGCGAGGGCTCTACTGGACCCCTCA 286
 QY 1279 atggtcgccgctgcctctgagctgctccgctcttaacacccctccacccctggccctgg 1338
 DB 287 ATGGCGCGCGCTGCGCCCTGAGCTCTCCGCTGACTCAAGCCCTCCACCTGGCTCTGG 346
 QY 1339 cctcgcttaacctaataaggtccagcagcagtcagagacaatctgtgtgtcagcgcc 1398
 DB 347 CCTGGCCCAACCTCAATGGGTCAGGACGCGGTGCGGGGACAACTCTGTGTGCGCACGCC 406
 QY 1399 gagacggcagcattctggctggctcctgcctctatgttggc 1439
 DB 407 GTGACGGCAGCATCTGCGTGGCTCTGCTCTATGTGGC 447

RESULT 11

V70895
 ID V70895 standard; cDNA; 1813 BP.
 AC V70895;
 DT 17-MAR-1999 (first entry)
 DE CDNA encoding an allelic variant of human Zcytor5.
 KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; Zcytor5 ligand; allelic variant;
 KW ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 88..1365
 FT /tag- a
 FT /product= Zcytor5
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.

PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 13-FEB-1998; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZIMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR P-PSDB; W0861.
 DR P-PSDB; W0861.
 PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
 PT down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Disclosure: Page 68-70; 55pp; English.
 CC The present sequence encodes an allelic variant of protein designated
 CC Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be
 CC administered to down-regulate the effects of a growth and/or maintenance
 CC factor in thyroid, heart, and skeletal muscle for example to lessen the
 CC effect of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible Zcytor5 ligands. A probe
 CC comprising Zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytor5 and
 CC therapeutically to modify Zcytor5 ligand effects.
 SQ Sequence 1813 BP; 415 A; 604 C; 519 G; 275 T;

Query Match 3.3%; Score 221.8; DB 1; Length 1813;
 Best Local Similarity 86.8%; Pred. No. 1.le-48;
 Matches 244; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1159 acacagctgtaatacagcccccagaccacccctctcatggtctccctcgaaagcta 1218
 DB 200 ACACAGCTGTGATCAGTCCCGAGGATCCACGCTTCTCATCGGCTCTCCCTGCGGCA 259
 QY 1219 cctgctctatacatgagacacacacccctggccagcctgaggggtctactggacctca 1278
 DB 260 CCTGCTCAGTGCAGCAGAGACCCACCCAGGAGCCACCGCGAGGGCTCTACTGGACCCCTCA 319
 QY 1279 atggtcgccgctgcctctgagctgctccgctcttaacacccctccacccctggccctgg 1338
 DB 320 ATGGCGCGCGCTGCGCCCTGAGCTCTCCGCTGACTCAAGCCCTCCACCTGGCTCTGG 379
 QY 1339 cctcgcttaacctaataaggtccagcagcagtcagagacaatctgtgtgtcagcgcc 1398
 DB 380 CCCGTGGCCAACTCAATGGGTCCAGGAGCGGTGCGGGGACAACTCTGTGTGCGCACGCC 439
 QY 1399 gagacggcagcattctggctggctcctgcctctatgttggc 1439
 DB 440 GTGACGGCAGCATCTGCGTGGCTCTGCTCTATGTGGC 480

RESULT 12

V41689
 ID V41689 standard; cDNA; 1579 BP.
 AC V41689;
 DT 26-OCT-1998 (first entry)
 DE Nucleotide sequence of the human U4 gene.
 KW Human; U4 protein; haematopoietin receptor superfamily;
 KW cell proliferation; immune response; antibody; cell differentiation;
 KW autoimmune disease; cancer; allergy; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..1228
 FT /tag- a
 FT /product= "U4 protein"
 PN WO9831811-A1.
 PD 23-JUL-1998.
 PF 15-JAN-1998; U00334.
 PR 16-JAN-1997; US-784863.
 PA (GEM) GENETICS INST INC.
 PI Collins M, Donaldson DD, Neben T, Whitters M;
 DR WPI; 98-414109/35.

CC maintenance or regeneration in an array of different cells and tissues in
CC vitro and in vivo. They can be present in therapeutics used for
CC modulating neuronal proliferation, differentiation and survival. The
CC products can also be used for detection and diagnosis, e.g. for cancers
CC or predisposition to cancers, or for drug screening.
SQ Sequence 560 BP; 113 A; 182 C; 165 G; 100 T;

Query Match 2.1%; Score 141.2; DB 1; Length 560;
Best Local Similarity 92.0%; Pred. No. 1.2e-27;
Matches 149; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 3434 gtaccacgagaccccccacccgacgtgacgtgagccgcttggtggggccctggaggaccag 3493
DB 382 GTGACACGAGACCCCGCCGCGACGTGACGTGAGCGCGCTGGGGGCGCTGGAGGACCA 441
QY 3494 ctgagtgctgctgggtctcaccacagctctcaagattctcttccaagccaagtac 3553
DB 442 CTGAGCGTGGCGTGGGTGTCGCCACCGCCCTCAAGGATTTCTTTTCAAGCCAAATAC 501
QY 3554 cagatccgtaccgctggtggaggacgctggtgactggaaggtg 3595
DB 502 CAGATCCGCTACCGAGTGGAGGACAGTGTGGATGGAGGTG 543

RESULT 15

X23316/C
ID X23316 standard; DNA; 4105 BP.
AC X23316;
DT 11-JUN-1999 (first entry)
DE Mouse 1-alpha-OHase promoter region DNA #2.
KW 1-alpha-OHase; vitamin D 1-alpha-hydroxylase; vitamin D pathway;
KW renal cytochrome P450 enzyme; 25-hydroxyvitamin D; human; mouse; rat;
KW diagnosis; treatment; disorder; endocrine; promoter; ss.
OS Mus sp.
PN W09907835-A2.
PD 18-FEB-1999.
PF 06-AUG-1998; CA0758.
PR 06-AUG-1997; US-906791.
PA (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.
PI Glorieux FH, St-Arnaud R;
DR WPI; 99-190048/16.
PT New polynucleotides encoding 25-hydroxyvitamin D 1-alpha-hydroxylase -
PT useful to detect and treat vitamin D-related disorders
PS Example 4; Page 79-81; 85pp; English.
CC This invention describes novel 25-hydroxyvitamin D 1-alpha-hydroxylase
CC (1-alpha-OHase), a renal cytochrome P450 enzyme of the vitamin D
CC pathway, and polynucleotides encoding the enzyme from human, mouse and
CC rat tissue. Molecules of the invention are used to diagnose and treat
CC Vitamin D-related disorders, to produce vitamin D metabolites, and to
CC identify modulators of the enzyme expression. The invention describes
CC an animal cell transformed with the enzyme promoter which is used to
CC identify compounds which modulate activity of the polynucleotide
CC encoding the enzyme, and to modulate the production of vitamin D in
CC patients with vitamin D endocrine disorders in the vitamin D
CC hydroxylation pathway, the enzyme catalyses conversion of
CC 25-hydroxyvitamin D to 1 alpha 25(OH)2D3.
SQ Sequence 4105 BP; 1063 A; 1032 C; 1063 G; 947 T;

Query Match 1.6%; Score 108.4; DB 1; Length 4105;
Best Local Similarity 74.3%; Pred. No. 1.8e-18;
Matches 150; Conservative 0; Mismatches 51; Indels 1; Gaps 1;
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DB 3580 TTTACCTTTTATCTATTGATTTTAGAGTCACTGTGGGGTTTTTTGTTGTTT 3521
QY 387 gagtttgtttattgtgacaggctctctgtgtagtctgctgctggaactcac 446
DB 3520 GTTTTGTGGTTTCCAGACAGAGGGTTTCTCTGTGTACCCCTGGCTGTC-TCGAACTCAC 3462
QY 447 tctgtagaccaggtggccttgaaactcagaaatccgcctgtgtgttcttcccaagtgtt 506

DB 3461 TCTGTAGACACGCTGGCCATCAAGAAATCAGCTGCTGCTCCCAAGTCTG 3402
QY 507 agattaaaggtgtgactgcca 528
DB 3401 GGATTAAGGCGTGCACCACCA 3380
Search completed: September 28, 1999, 16:50:24
Job time: 7609 sec

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1634 Std Error: 0.00
seq primer: -40UP from Gibco

NID g1375694
 VERSION W66776.1 GI:1375694
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 REFERENCE 1 (bases 1 to 482)
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Stepcoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
 TITLE The WashU-HHMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT On Apr 14, 1993 this sequence version replaced gi:785250.
 Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:239573
 Possible reversed clone: similarity on wrong strand
 Seq primer: ETPRimer
 High quality sequence stop: 359.
 Location/Qualifiers
 1. 482
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 /sex="unknown"
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 /lab_host="DH10B"
 /note="vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGAGATTTTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru KO, Wayne State Univ., from 2]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
 BASE COUNT 96 a 138 c 147 g 101 t
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 Query Match 3.2%; Score 214.8; DB 26; Length 482;
 Best Local Similarity 81.1%; Pred. NO. 1.3e-42;
 Matches 305; Conservative 0; Mismatches 2; Indels 69; Gaps 2;
 QY 3434 gtgaccacgagccccaccacacgtgacgtgacggtggggcctgagaccag 3493
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 DB 257 CTGAGTGTGCGTGGGTCTCACACCAGCTCTCAAGGATTTCCTCTCTCCAGCCAGTAC 198
 QY 3554 cag-atccgctaccgctgagagacagcgtgagctggaggtgcctcccccgcgcgac 3612
 DB 197 CAGTATTCTGCTACCGCGTGGAGGACAGCGTGGACTGGA----- 159

QY 3613 cgcacctgacccgcccccccgcatctgactctcctcaccgtgcaggtgggtgatgac 3672
 DB 159 -----AGGTGGTGGATGAC 146
 QY 3673 gtcaagaacacagacctctcctgcctctcgcgggctgaagcccgccaccttactcgtc 3732
 DB 145 GTCAGCAACAGACACCTCTCTGCCGTCTCGCGGGCTGAAGCCCGCCACCGCTTTACTTCGTC 86
 QY 3733 caagtgcgtgttaacccattcgggattctatggtcgaataaagcgcgaatcctgagacgag 3792
 DB 85 CAAGTCGCTGTAAACCATTCGGGATCTATGGTCTGAAAAGCGGGAATCTCGAGCGGAG 26
 QY 3793 tggagccacccaccg 3808
 DB 25 TGGAGCCACCCCATCG 10
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 LOCUS AV032198 262 bp mRNA EST 03-JUN-1999
 DEFINITION AV032198 Mus musculus adult C57BL/6J cerebellum Mus musculus cDNA clone 1500034F20, mRNA sequence.
 ACCESSION AV032198
 NID 94831746
 VERSION AV032198.1 GI:4831746
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 262)
 AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Ito, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y., Tomimaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 RIKEN Mouse ESTs
 Unpublished (1999)
 COMMENT On Jun 22, 1998 this sequence version replaced gi:3246782.
 Contact: Chile Owa
 Genome Science Laboratory
 RIKEN
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098
 Email: genome-res@rtc.riken.go.jp
 Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998)).
 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998)).
 Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
 Location/Qualifiers
 1. 262
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="1500034F20"
 /clone_lib="Mus musculus adult C57BL/6J cerebellum"
 /sex="male"
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 BASE COUNT 63 a 63 c 69 g 67 t
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 Query Match 3.2%; Score 213; DB 50; Length 262;

Best Local Similarity 93.54; Pred. No. 3e-42;
Matches 244; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

Qy 6364 caggctctgcgcggctaaactaaagcctagccatctctcct-gctgggtcagacctgag 6422
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Db 2 CACGTTCTCGGGGGTAACTATTAGATCGGCTATCCCTTCGCTGGGTAGACCTGGAG 61
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Qy 6423 gtcacctgaattggagccctctgtaccatctgggcaacaagaacctaccagagct 6482
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Db 62 GCTCACCTGAATTGGAGCCCTTTGTACCAATTTGGCAACAAGAAACCTACCAGAGCT 121
|||||
Qy 6483 -gggcacaatgagctcccaacaacacagcttgggtccacatgatggtcacacttggatat 6541
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Db 122 GGGCACAATGAGTCCCAACACACAGCTTTGGTCCACATGATGGTCACACTTGGATAT 181
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Qy 6542 acccagctgggttaggggtgggtattgcaggccctcccaagagctctcttaataaat 6601
|||||
Db 182 ACCCCAGTGGGTAGGGTGGGGTATTCGAGGCGCTCCCAAGAGTTCCTTTAAATAAAT 241
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Qy 6502 aaaggagttgtcaggtcccg 6622
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Db 242 AAAGGAGTTGTTCAAGTCCCG 262
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RESULT 14
AI574687
LOCUS
DEFINITION
ACCESSION
NID
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

AI574687 319 bp mRNA EST 30-MAR-1999
UI-R-G0-uc-b-11-0-UI.s1 UI-R-G0 Rattus norvegicus cDNA clone
UI-R-G0-uc-b-11-0-UI 3', mRNA sequence.
AI574687
94544683
AI574687.1 GI:4544683
EST.
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 319)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704477
On May 18, 1998 this sequence version replaced gi:3138307.

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares-Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward.
Location/Qualifiers
1..319
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/clone="UI-R-G0-uc-b-11-0-UI"
/clone_lib="UI-R-G0"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-G0
library is a normalized library constructed from a
mixture of rat tissues (nodose ganglia, dorsal root
ganglia, and trigeminal ganglia). The tag is a string of
6 nucleotides present between the Not I site and the

FEATURES
source

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACATCTGAGTCGAGCGCCGCGCATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fátima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

BASE COUNT
ORIGIN

	Query Match	3.0%	Score	200.2;	DB	26;	Length	390;
	Best Local Similarity	97.4%;	Pred. No.	5.1e-39;				
	Matches	225;	Conservative	0;	Mismatches	3;	Indels	3;
								Gaps
								2;
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QY	6425	tcacctgaattggagccctctgtaccatctgggcacacaaagaaacctaccagagct-g	6483					
Db	220	TCACCTGAATTGGAGCCCTCTGTACCATCTGGGCACAAAGAAACCTACCGAGGCTGG	279					
QY	6484	ggcacaaatgagctcccaacacacagatttgggtccacatgatgggtcacacttgggtatcac	6543					
Db	280	GGCACAAATGAGTCCACACACCACAGCTTTGGTCCACATGATGGTCACACTGGATATAC	339					
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Search completed: September 28, 1999, 15:38:38
Job time: 3306 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 28, 1999, 15:38:23 ; Search time 2095.87 Seconds
(without alignments)
6270.900 Million cell updates/sec

Title: US-09-037-657-28

Perfect score: 6663

Sequence: 1 cccgaactcttgacgactg.....tatgtctgggtggggga 6663

Scoring table: IDENTITY_NUC

Searched: 2546578 seqs, 986266752 residues

Database :

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3: em_est3:*
4: em_est4:*
5: em_est5:*
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57: em_est25:*
58: em_est26:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	248	3.7	445	27	AA039053	AA039053 m199d07.r
2	221.8	3.3	462	45	AI394468	AI394468 tf79d12.x
3	221.8	3.3	474	46	AI421423	AI421423 tf25h01.x
4	220.2	3.3	466	43	AI161002	AI161002 qb69d04.x
5	220.2	3.3	466	43	AI185780	AI185780 qb44h04.x
6	220.2	3.3	477	43	AI185924	AI185924 qb50c05.x
7	220.2	3.3	447	43	AI187074	AI187074 qb38a03.s
8	220.2	3.3	417	44	AI269388	AI269388 q126b05.x
9	219.6	3.3	332	48	AI579568	AI579568 UI-R-GO-u
10	219.2	3.3	431	45	AI333812	AI333812 qp93e12.x
11	215.4	3.2	385	50	AI670108	AI670108 w655f03.x
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13	213	3.2	262	50	AV032198	AV032198 AV032198
14	207.2	3.1	319	48	AI574687	AI574687 UI-R-GO-u
15	200.2	3.0	390	26	W17583	W17583 mb75b01.r1
16	195.6	2.9	410	27	AA042914	AA042914 z456f01.s
17	176.8	2.7	273	23	R87407	R87407 ym88d09.s1
18	174.8	2.6	464	29	AA049280	AA049280 m145d02.r
19	171	2.6	428	45	AA866388	AA866388 UI-R-AO-a
20	169.4	2.5	229	49	AV010798	AV010798 AV010798
C 21	164	2.5	503	29	AA049278	AA049278 m145c04.r
22	160.4	2.4	465	26	W46604	W46604 zc32h10.s1
C 23	159.2	2.4	455	46	AA925924	AA925924 UI-R-A1-e
C 24	151	2.3	470	43	AI233311	AI233311 EST229999
25	143.8	2.2	167	49	AV011309	AV011309 AV011309
C 26	135.8	2.0	464	41	AI071408	AI071408 UI-R-C2-d
27	134.8	2.0	235	48	AI575060	AI575060 UI-R-GO-u
28	124	1.9	422	46	AI451475	AI451475 mu42a09.x
C 29	123	1.8	458	27	AA043001	AA043001 zK56f01.r
C 30	121.4	1.8	309	48	AI597540	AI597540 v075b01.y
31	117.4	1.8	433	38	AA760301	AA760301 v075b01.y
32	116.6	1.7	771	49	AI648748	AI648748 uk28a02.x
33	115.4	1.7	546	40	AA986345	AA986345 uc79a05.x
34	114.6	1.7	406	46	AI414045	AI414045 ma04c06.x
35	113.8	1.7	460	42	AI115029	AI115029 u146d12.x
36	113.6	1.7	512	42	AI131774	AI131774 ue96c09.x
37	113.4	1.7	220	28	AA067965	AA067965 mm24h01.r
38	113	1.7	460	41	AI047521	AI047521 ud61h02.x
39	113	1.7	444	43	AI173940	AI173940 uf05g08.x
C 40	112.4	1.7	342	36	AA608095	AA608095 vm55c07.r
C 41	112.4	1.7	422	37	AA883670	AA883670 vr03e10.r
42	112.2	1.7	558	36	AA611861	AA611861 v082c08.r
43	112.2	1.7	362	47	AI505025	AI505025 v195d05.x
44	112	1.7	323	47	AI506426	AI506426 vm55c07.x
C 45	111.4	1.7	377	38	AA792160	AA792160 vn71b10.r

ALIGNMENTS

RESULT 1
AA039053/c
LOCUS m199d07.r1 Soares mouse embryo NbMEL3.5 14.5 Mus musculus cDNA
DEFINITION clone IMAGE:474733 5', mRNA sequence.
ACCESSION AA039053
NID GI1514788
VERSION AA039053.1 GI:1514788

KEYWORDS
SOURCE
ORGANISM

EST.
Mus musculus
house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 445)
Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
Geisler S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
Schellenberg K., Stepcoe M., Tan F., Underwood K., Moore B.,
Theising B., Wyllie T., Lennon G., Soares B., Wilson R. and
Waterston R.
TITLE
The WashU-HMI Mouse EST Project
JOURNAL
Unpublished (1996)
COMMENT

Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:285477
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 441.

FEATURES
source

Location/Qualifiers
1. 445
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:474733"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGGAGCGGCGGAAATTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
p7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."
BASE COUNT 85 a 129 c 124 g 107 t
ORIGIN

Query Match 3.7%; Score 248; DB 27; Length 445;
Best Local Similarity 99.6%; Pred. No. 8.1e-51;
Matches 259; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 6365 aggtccctgcggctaaactaagatagccatctcctgctgggtcagacacctggagc 6424
Db 265 AGGCTCTGGCGCTAAACTCTAAGATAGCCATCTCTCTGCTGGGTACACCTGGAGGC 206
Qy 6425 tcacctgaattggagccctctgtaccatctgggcaacaagaacctaccagggtct-g 6483
Db 205 TCACCTGAATTGGAGCCCTCTGTACCATCTGGGCAACAAGAACCTACAGAGGCTGG 146
Qy 6484 ggcacaatgacctcccaaccacagcttgggtccacatgatggtcacattggatatac 6543
Db 145 GGCACAATGAGCTCCCAACACAGAGCTTTGGTCCCATGATGCTACATCTGGATATAC 86
Qy 6544 cccagtggtgtaggttggtggtattgcaggggcctcccaagagctcttttaataataa 6603
Db 85 CCCAGTGTGGGTAGGTTGGGTATTGCGAGGGCCTCCCAAGAGTCTCTTTAAATAATA 26

QY 6604 aggagttgttcagggtcccca 6623
|||||
Db 25 AGGAGTTGTTCAGGTCCCGA 6

RESULT 2

AI394468
LOCUS
DEFINITION
AI394468 462 bp mRNA EST 30-MAR-1999
mrna sequence. CDNA clone IMAGE:2105495 3',
ACCESSION
AI394468
VERSION
94224015
KEYWORDS
AI394468.1 GI:4224015
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 462)
AUTHORS
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
JOURNAL
Unpublished (1998)
COMMENT
On Feb 17, 1998 this sequence version replaced gi:2887603.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1631 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 454.

FEATURES
source

Location/Qualifiers
1. 462
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="10; 1"
/clone="IMAGE:2105495"
/clone_lib="NCI-CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: p7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGGAGCGGCGGAAATTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 79 a 181 c 122 g 79 t
ORIGIN

Query Match 3.3%; Score 221.8; DB 45; Length 462;
Best Local Similarity 86.6%; Pred. No. 2.5e-44;
Matches 244; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
Qy 1159 acacagcttaacagcccccagaccacccatcttcctcgctcctccctgcaagcta 1218
Db 54 ACACAGCTGTGATCAGTCCCCCAGGATCCACAGCTTCTCATCGGCTCCTCCCTGCTGCCA 113
Qy 1219 cctgctctacatgagacacacacctggggccacgctgagggctctactgaccttca 1278

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 28, 1999, 16:46:12 ; Search time 3489.95 Seconds
(without alignments)
31.895 Million cell updates/sec

Title: US-09-037-657-30
Perfect score: 35
Sequence: 1 agctggcgccctccggcgccgagccac 35

Scoring table: IDENTITY_NUC

Searched: 679419 seqs, 1590154680 residues

Database :

GenEmbl:**
1: gb_ba1:**
2: gb_ba2:**
3: gb_om:**
4: gb_ov:**
5: gb_pat:**
6: gb_ph:**
7: gb_pl1:**
8: gb_pl2:**
9: gb_pr1:**
10: gb_pr2:**
11: gb_pr3:**
12: gb_ro:**
13: gb_st:**
14: gb_sts:**
15: gb_sy:**
16: gb_un:**
17: gb_vi:**
18: em_fun:**
19: em_htg:**
20: em_hum1:**
21: em_hum2:**
22: em_in:**
23: em_om:**
24: em_or:**
25: em_ov:**
26: em_pat:**
27: em_ph:**
28: em_pl:**
29: em_ro:**
30: em_sts:**
31: em_sy:**
32: em_un:**
33: em_vi:**
34: gb_htgl:**
35: gb_htg2:**
36: gb_in1:**
37: gb_in2:**
38: em_ba1:**
39: em_ba2:**
40: em_hum3:**
41: em_hum4:**
42: gb_pr4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	35	100.0	35	5	A70400	A70400 Sequence 30

C 2	22.2	63.4	3885	12	MMBRADPR	Y07919 M.musculus
C 3	22.2	63.4	195923	35	AC005528	AC005528 Mus muscu
C 4	21.8	62.3	43839	1	MLCL458	AL049478 Mycobacte
C 5	21.8	62.3	42923	1	MSGB13GS	L78823 Mycobacteri
C 6	21.4	61.1	2188	1	STMTLP	D30760 Streptomyce
C 7	21.4	61.1	239	10	HSDNASGAT	Z22412 H.sapiens D
C 8	21.4	61.1	239	10	HSNL2273D	X87522 H.sapiens g
C 9	21.2	60.6	111746	9	HS327J16	AL008583 Human DNA
C 10	21.2	60.6	315	10	HSZ94778	Z24778 H.sapiens g
C 11	21.2	60.0	348	10	HSDNASIAO	Z2459 H.sapiens D
C 12	20.6	58.9	5137	1	PFQOQACBF	X87299 P.fluoresce
C 13	20.4	58.3	41055	1	SC6G4	AL031317 Streptomy
C 14	20.4	58.3	1506	9	D86087S01	D86087 Human DNA f
C 15	20.4	58.3	133221	10	HS333A15	AL031429 Human DNA
C 16	20.4	58.3	187943	35	AC007226	AC007226 Homo sapi
C 17	20.2	57.7	1600	1	AB015626	AB015626 Streptomy
C 18	20.2	57.7	1629	5	A70382	A70382 Sequence 12
C 19	20.2	57.7	1673	5	A70384	A70384 Sequence 14
C 20	20.2	57.7	1930	5	A70392	A70392 Sequence 22
C 21	20.2	57.7	173140	34	AC004867	AC004867 Homo sapi
C 22	20.2	57.7	227571	34	AC005098	AC005098 Homo sapi
C 23	20.2	57.7	167700	34	AC005488	AC005488 Homo sapi
C 24	20.2	57.7	125815	34	HS436C18	AL031301 Homo sapi
C 25	20.2	57.7	281498	35	AC004166	AC004166 Homo sapi
C 26	20.2	57.7	127759	42	AC006014	AC006014 Homo sapi
C 27	20	57.1	4509	1	RHMSNAD	M14052 R.mellotti
C 28	20	57.1	4110	1	RHNODEFG	Y06604 Rhizobium m
C 29	20	57.1	3932	1	RMNODEFG	X04379 Rhizobium m
C 30	20	57.1	38252	11	AC004463	AC004463 Homo sapi
C 31	19.8	56.6	39150	1	MTCY164	Z95150 Mycobacteri
C 32	19.8	56.6	608	2	AF126478	AF126478 Mycobacte
C 33	19.8	56.6	238	7	CTRIDITS1	Z72280 C.tridentat
C 34	19.8	56.6	2711	9	HS415521	Y15521 Homo sapien
C 35	19.8	56.6	80141	10	HSEWSGAR	Y07848 Homo sapien
C 36	19.8	56.6	126322	11	AC000026	AC000026 Homo sapi
C 37	19.8	56.6	3679	12	RATBCCAPA	M77245 R.norvegicu
C 38	19.8	56.6	225021	34	CNS0000H	AL049836 Homo sapi
C 39	19.8	56.6	173029	42	AC002059	AC002059 Homo sapi
C 40	19.6	56.0	6394	1	AB014348	AB014348 Rhodococc
C 41	19.6	56.0	1560	1	RMD44891	U44891 Rhodococcus
C 42	19.6	56.0	39461	1	SC6A9	AL031035 Streptomy
C 43	19.6	56.0	2712	1	STMPAB	M64859 S.lividans
C 44	19.6	56.0	63734	2	AF127374	AF127374 Streptomy
C 45	19.6	56.0	931	3	OCTF02	AF031612 Oryctolag

ALIGNMENTS

RESULT 1	A70400	Sequence 30 from Patent WO9811225.	35 bp	DNA	PAT	07-MAY-1999
LOCUS	A70400	Sequence 30 from Patent WO9811225.				
DEFINITION	A70400	Sequence 30 from Patent WO9811225.				
ACCESSION	A70400	Sequence 30 from Patent WO9811225.				
NID	94774677	GI:4774677				
VERSION	A70400.1	GI:4774677				
KEYWORDS		unidentified.				
SOURCE		unidentified.				
ORGANISM		unclassified.				
REFERENCE	1	(bases 1 to 35)				
AUTHORS		Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S., Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and Kikuchi,Y.				
TITLE		A NOVEL HAMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME				
JOURNAL		Patent: WO 9811225-A 19-MAR-1998;				
FEATURES		NICOLA NICOS ANTONY (AU)				
source		Location/Qualifiers				
		1..35				
		/organism="unidentified"				
		/db_xref="taxon:32644"				
BASE COUNT	4 a	14 c	14 g	3 t		
ORIGIN						

Query Match 100.0% Score 35; DB 5; Length 35;
 Best Local Similarity 100.0%; Pred. No. 0.082;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agctggcgccctcccgccgagatcgaggagccac 35
 |||||
 Db 1 AGTGCGGCGCTCCCGCGGATCGGAGCCAC 35

RESULT 2
 MMBPRADPR/c
 LOCUS MMBPRADPR 3885 bp mRNA ROD. 10-SEP-1997
 DEFINITION M.musculus mRNA for beta-prime-adaptin protein.
 ACCESSION Y07919
 NID 92398719
 VERSION Y07919.1 GI:2398719
 KEYWORDS beta-prime-adaptin protein.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 3885)
 AUTHORS Guilbaud, C., Fransson, I., Clifton, S.W., Roe, B.A., Carter, N. and
 Dumanski, J.P.
 TITLE Characterization of a mouse homologue for human beta-prime-adaptin
 gene: cDNA sequence, genomic structure and chromosomal localization
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 3885)
 AUTHORS Guilbaud, C.
 TITLE Direct Submission
 JOURNAL Submitted (11-SEP-1996) C. Guilbaud, Dept. Of Molecular Medicine,
 Clinical Genetics Unit, Karolinska Hospital, Building L-6, S-171 76
 Stockholm, SWEDEN

FEATURES
 source
 1. 3885
 /organism="Mus musculus"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /chromosome="11"
 /clone_lib="whole mouse embryo"
 /clone_lib="mouse brain"
 /clone="gt3"
 /clone="351"
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 /codon_start=1
 /product="beta-prime-adaptin protein"
 /protein_id="CAA69224.1"
 /db_xref="PID:g266088"
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 /db_xref="GI:2398720"
 /db_xref="MGD:MGI:1096368"
 /db_xref="SPTREMBL:O35643"
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 KVSALFPDVNMCOTDNLKLVLYLMYAKSPDMAIMAVNTFVKDCEDNPDI
 RALAVTGCIRVDKITEYLCPELRKCLKDEDPYVRKTAACVAKLHDINAQLVEDG
 ELDTLKDILSDNPMVANAVALSEIAESHPSSNLLDLNPSQINKLLTALNECTEG
 QIFLDCDNDNPKDREAQSCICERTPLRSHANSVAVLSAVKLMKFMELSKDLDY
 YATLKKLAPPLVTLTSLAEPLQYVALRNILIVQKREPLKHEKVFYKNDPIYV
 KLEKIDIRLASQANIAQVLAELKAYEATVDVDFKRAVRAICAKLKVQSAERCV
 STLLDQTKVNVVQEAIVKIDIFRYPNKYESVIATVLCENLSDLEPEARAAMIV
 IVGEAERIDNADELSEFLGFDHESQVQLTLTAVKLEKPTQELVQVLS
 LATQSDNPLDRGYIYRLLSTIDPVAKEVLAKEPLISEEDLIEPTLLELICI
 IGTLSVHKPNAEVEGGRVVHKSLLPRTASSESTESPETAPAGAPGPODPIPA
 OGDLLDNLNLDLPGPPPLAASVQGVAVDGLGGLDLSLDGNSFGAPASVAA
 PAPARLAP ISSGLSLEFLTSGVGLSGSVYPAKVALPAMKAKGLISGFTFROAG
 STSMQLQTNALQVMTDFAIQFNRSNFGAPAAPLOVHPLSPNOTVEISLPTNVC
 SYLKEPLNNQVAVKNNIDVFYETFLPLVLFVDEGKMDROMFLATWKIDANEA
 OFQIRDCPLNTEAASNKLOSNIFVARNVEGGQMLYQSLKINGIHWLAELRIQPG
 NPSFTLSKRAPEVSQHVQIAETILKAN"
 929 a 1050 c 1045 g 861 t

BASE COUNT
 ORIGIN

Query Match 63.4% Score 22.2; DB 12; Length 3885;
 Best Local Similarity 77.1% Pred. No. 1.9e+02;
 Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 agctggcgccctcccgccgagatcgaggagccac 35
 |||||
 Db 3067 ATCAGGGAGGCTCCTCGGTGTTTCAGGAGCCAC 3033

RESULT 3
 AC005528/c
 LOCUS AC005528 195923 bp DNA HTG 29-MAY-1999
 DEFINITION Mus musculus, WORKING DRAFT SEQUENCE, 7 ordered pieces.
 ACCESSION AC005528
 NID 94926879
 VERSION AC005528.10 GI:4926879
 KEYWORDS HTG; HTGS_PHASE2.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 195923)
 AUTHORS Fang, F., Ying, F., Pan, H., Dumanski, J. and Roe, B.A.
 TITLE Unpublished
 JOURNAL Mus musculus PAC Clone 493n6 In MDR Region
 REFERENCE 2 (bases 1 to 195923)
 AUTHORS Fang, F., Ying, F., Pan, H., Dumanski, J. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (25-AUG-1998) Department Of Chemistry And Biochemistry,
 The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019 USA

On May 29, 1999 this sequence version replaced gi:4510435.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 7 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * been provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved
 * 1 2246: contig of 2246 bp in length
 * 2247 2316: gap of unknown length
 * 2317 6162: contig of 3846 bp in length
 * 6163 6232: gap of unknown length
 * 6233 24021: contig of 17789 bp in length
 * 24022 24091: gap of unknown length
 * 24092 46425: contig of 22334 bp in length
 * 46426 48495: gap of unknown length
 * 48496 73433: contig of 26938 bp in length
 * 73434 73504 103517: gap of unknown length
 * 73504 103518 103587: contig of 30014 bp in length
 * 103588 195923: contig of unknown length
 * 103588 195923: contig of 92336 bp in length.

FEATURES
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 1. 195923
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 BASE COUNT 50392 a 48306 c 47825 g 48972 t 428 others
 ORIGIN

Query Match 63.4% Score 22.2; DB 35; Length 195923;
 Best Local Similarity 77.1% Pred. No. 69;
 Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 agctggcgccctcccgccgagatcgaggagccac 35
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 Db 125043 ATCAGGGAGGCTCCTCGGTGTTTCAGGAGCCAC 125009


```

RESULT 4
MCL458
LOCUS MCL458 43839 bp DNA BCT 24-MAR-1999
DEFINITION Mycobacterium leprae cosmid L458.
ACCESSION AL049478
NID 94539121
VERSION AL049478.1 GI:4539121
KEYWORDS acp; CoA:apo-[AcyI Carrier Protein]; DNA polymerase III alpha chain; dnaE; fas; ila; ilvA; isoleucyl-tRNA synthetase; L-asparaginase; L-glutaminase; lipoprotein signal peptidase; lspa; oxidoreductase; pseudogene; pseudouridine synthase; RLEP element; rluC; threonine dehydratase biosynthetic; type I fatty acid synthase.
SOURCE Mycobacterium leprae.
ORGANISM Mycobacterium leprae
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 43839)
Eiglmeyer,K., Honore,N., Woods,S.A., Caudron,B. and Cole,S.T.
Use of an ordered cosmid library to deduce the genomic organization of Mycobacterium leprae
Mol. Microbiol. 7 (2), 197-206 (1993)
93188700
2 (bases 1 to 43839)
Seeger,K.J. and Harris,D.
Unpublished
3 (bases 1 to 43839)
James,K.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
Submitted (15-MAR-1998) Mycobacterium leprae sequencing project, CB10 ISA E-mail: barrellesanger.ac.uk Cosmids Cambridge Stewart T. Cole, [3] Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France Requests for cosmids should be sent to Karin Eiglmeyer (keiglmeyer@pasteur.fr)
Notes:
The Sanger Centre is funded to complete the sequence of M. leprae by the Heiser Program for Research in Leprosy and Tuberculosis of The New York Community Trust.
Work in Paris is supported by the Heiser Trust, the Association Française Raoul Follereau and the Groupement de Recherches et des Etudes des Genomes (GIP-GREG).
Details of M. leprae sequencing at the Sanger Centre are available on the World Wide Web.
(URL, http://www.sanger.ac.uk/projects/)
CDS are numbered using the following system eg MLCB33.01c. ML (M. leprae), cB33 (cosmid name), .01 (first CDS), c (complementary strand).
The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.
Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. All CDS over 100 codons have been analysed. Gene prediction is based on positional base preference in codons especially where there is an increase in the observed/expected third position G + C. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
Location/Qualifiers
1. .43839
/organism="Mycobacterium leprae"
/db_xref="taxon:1769"

FEATURES
source
/clone="cosmid L458"
1. .569
/note="overlap with cosmid B1701 from 19932 to 20500"
complement(97..531)
/gene="MLCB485.01c"
complement(97..531)
/gene="MLCB485.01c"
/note="MLCB485.01c, hypothetical protein, len: 114 aa; unknown function, possible CDS based on amino acid composition and frame analysis"
/codon_start=1
/transl_table=11
/label="MLCB485.01c"
/product="hypothetical protein MLCB485.01c"
/protein_id="CAB39568.1"
/db_xref="PID:e1419859"
/db_xref="PID:g4539122"
/db_xref="GI:4539122"
/translation="MQSLRRHFTCRSTFYHGYSILPAQRAVVRTSTADTHLSDTWTCGA
AGENQRTNHPADVONVGRLLSGSVTYTPAPRSVGRVTSPPADLLDDSFCHSGTNPFLLD
QVAVFPADLKPQLRNTAKRAVDHGHEVQWLDVFAWVPP"
complement(827..1210)
/gene="MLCB458.02c"
complement(827..1210)
/gene="MLCB458.02c"
/note="MLCB458.02c, hypothetical protein, len: 127 aa; unknown function, N-terminus similar to internal sequence of TP22_MYCTU (EMBL:Z80226) RV0778 (MTCY369.22) M. tuberculosis hypothetical protein (414 aa), fasta scores: opt: 139 z-score: 189.2 E(): 0.0031, 31.4% identity in 102 aa overlap"
/codon_start=1
/transl_table=11
/label="MLCB458.02c"
/product="hypothetical protein MLCB458.02c"
/protein_id="CAB39567.1"
/db_xref="PID:e1419860"
/db_xref="PID:g4539123"
/db_xref="GI:4539123"
/translation="MLEKNRPQIFDSFDRILKARSPAWLSRRKEIDLHSTIFEYTLK
LTAEKRRNPDDIWRTLASAVITGNDEKPFRLPANELLEFFVLFTGTSNAKTITGYW
TAGVHESRPDKTIPRSGSIAPQRR"
complement(1581..1850)
/gene="MLCB458.03c"
complement(1581..1850)
/gene="MLCB458.03c"
/note="MLCB458.03c, hypothetical protein, len: 89 aa; unknown function, improbable CDS based on frame analysis"
/codon_start=1
/transl_table=11
/label="MLCB458.03c"
/product="hypothetical protein MLCB458.03c"
/protein_id="CAB39568.1"
/db_xref="PID:e1419861"
/db_xref="PID:g4539124"
/db_xref="GI:4539124"
/translation="MLAPEWROGGEFVFTIAVKYVITLLSGHIQNGRTSSHRIEYSL
FLNHRHCLISSSSDGVGKSDDETRREPVSQRNTGRSELPF"
complement(1841..2110)
/gene="MLCB458.04c"
complement(1841..2110)
/gene="MLCB458.04c"
/note="MLCB458.04c, hypothetical protein, len: 89 aa; unknown function, possible CDS based on amino acid composition and frame analysis"
/codon_start=1
/transl_table=11
/label="MLCB458.04c"
/product="hypothetical protein MLCB458.04c"
/protein_id="CAB39569.1"
/db_xref="PID:e1419862"
/db_xref="PID:g4539125"
/db_xref="GI:4539125"

```

```

/translation="MTERMTAWRIPIGKIAAREIPATALVNSVNPKIPLWPAESYRRM
RCDTTSYRVDSFSDSDVIDSHQSLSIIVAVERSAQIAQLAISGCS"
3625..4344
/gene="MLCB458.05"
CDS
3625..4344
/gene="MLCB458.05"
/note="MLCB458.05, possible secreted protein, len: 239 aa;
unknown function, similar to TR.P95028 (EMBL:283863)
RV2525c (MTC159.31) M.tuberculosis hypothetical protein
(240 aa), fasta scores; opt: 1358 z-score: 1535.9 E(): 0,
82.2% identity in 241 aa overlap. Contains possible
N-terminal signal sequence"
/codon_start=1
/transl_table=11
/label="MLCB458.05"
/product="hypothetical protein MLCB458.05"
/protein_id="CAB39570.1"
/db_xref="PID:e1419863"
/db_xref="PID:g4539126"
/db_xref="GI:4539126"
/translation="MSVSRDVLKFAITVTPGLGLGVAAALCAVPASTAGSLGTLDD
YAGVIFASQIRATGAVGAIKRVSDRGIWAVGKPIQVTEARDLNNGLKIVSCVOYGR
KGTADWLGGATAGLRHAQGVQLHTAAGPVSAPIASIDSNPTIYEQYKQVAPVLR
SWESVIGHQRTGYVANSRTIAWALQDLASIFWQHNWSPKGYTHPAANLHQVEIDRR
TVGGVGVNVNTILKPOFGWA"
4936..14186
/gene="fas"
CDS
4936..14186
/gene="fas"
/note="MLCB458.06, fas, probable type I fatty acid
synthase, len: 3076 aa; similar to many eubacterial and
eukaryotic FAS e.g. TR:Q59497 (EMBL:X87822) Brevibacterium
amonniogenes FAS (3063 aa), fasta scores; opt: 5361
z-score: 5527.0 E(): 0, 44.3% identity in 3106 aa overlap.
N-terminus shows similarity to FAS1_CANAL (EMBL:X74952)
Candida albicans FAS beta subunit (2037 aa) (27.3%
identity in 1928 aa overlap) and C-terminus to FAS2_CANAL
(EMBL:L29063) Candida albicans FAS alpha subunit (1885 aa)
(27.1% identity in 1739 aa overlap). C-terminus similar to
N-terminus of TR:O69474 (EMBL:AL023635) MLCB1243.20c,
kasa, M.leprae beta-ketoacyl-ACP synthase (414 aa) (27.5%
identity in 386 aa overlap) and TR:O69473 (EMBL:AL023635)
MLCB1243.19c, kasa, M.leprae beta-ketoacyl-ACP synthase
(425 aa) (25.1% identity in 382 aa overlap). Equivalent to
TR:P95029 (EMBL:283863) RV2524c (MTC159.32-WF008.09c)
M.tuberculosis FAS (3069 aa) (85.8% identity in 3081 aa
overlap). Contains pfam match to entry PF00698
Acyl.transf, Acyl transferase domain, score 18.20, E-value
1.9e-08, PS00017 ATP/GTP-binding site motif A (P-loop) and
PS00606 Beta-ketoacyl synthases active site"
/codon_start=1
/transl_table=11
/label="fas"
/product="putative type I fatty acid synthase"
/protein_id="CAB39571.1"
/db_xref="PID:e1419864"

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Query Match 62.3%; Score 21.8; DB 1; Length 43839;
 Best Local Similarity 78.8%; Pred. No. 1.3e+02;
 Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 gctggcgccctccggcgatcgaggagccca 34
 |||||
 Db 34722 GCTGGCGCGCCACCCCGGCACATCGCAAGTCCA 34754

RESULT 5
 MSGB13GS/c MSGB13GS 42923 bp DNA BCT 26-JUN-1996
 LOCUS Mycobacterium leprae cosmid B13 DNA sequence.
 DEFINITION L78823
 NID 91377768
 VERSION L78823.1 GI:1377768

KEYWORDS
 SOURCE Mycobacterium leprae (clone: cosmid B13) (tissue library: Lorist 6) DNA

ORGANISM
 Mycobacterium leprae
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 Actinomycetales; Corynebacterineae; Mycobacteriaceae;
 Mycobacterium.

REFERENCE
 1 (sites)
 Eiglmeyer, K., Honore, N., Woods, S.A., Caudron, B. and Cole, S.T.
 Use of an ordered cosmid library to deduce the genomic organization
 of Mycobacterium leprae
 Mol. Microbiol. 7 (2), 197-206 (1993)

JOURNAL
 MEDLINE 93188700
 REFERENCE
 2 (bases 1 to 42923)
 Smith, D.R., Richters, P., Rubenfield, M., Butler, C., Lee, H.-M.,
 Xu, Q., Gunderson, K., Chung, M., Maher, J.K., Deloughery, C.,
 Aldrich, T., Imrich, J., Tullig, C., Smyth, A., Drill, S., Avruch, A.S.,
 Rice, P., Abendschan, K., Aldredge, T., Deloughery, C., Kirst, S.,
 Safer, H., Connelly, S., McDougall, S., Eiglmeyer, K., Bergh, S.,
 Cole, S., Robison, K., Jaehn, L., Gryan, G., Church, G.M. and Mao, J.
 Prepublication submission
 Unpublished (1996)

JOURNAL
 COMMENT This sequence was generated by the Genome Sequencing Center at
 Genome Therapeutics Corporation (Collaborative Research Division),
 100
 Beaver St., Waltham, MA, 02154. Please contact Doug Smith
 (smith@eric.com) for further information. The sequence represents
 the
 insert of a Lorist 6 cosmid clone from a mapped set of clones
 constructed from M. leprae genomic DNA isolated from armadillo
 liver
 [3]. The sequence may not represent the entire cloned insert of
 the
 cosmid if an overlapping region was previously sequenced from
 another
 clone. Coding sequences larger than 60 amino acids were predicted
 on
 the basis of codon usage and homology information. An attempt was
 made
 to locate the most probable start site based on codon usage,
 the
 presence of a Shine-Dalgarno sequence, or overlapping orf that
 suggested translational coupling. It is possible that the actual
 start
 site differs from the one selected.

FEATURES
 source
 1..42923
 /organism="Mycobacterium leprae"
 /specific_host="Dasypus novemcinctus"
 /db_xref="taxon:1769"
 /clone="cosmid B13"
 /tissue_lib="Lorist 6"
 /note="The liver of the armadillo was used to isolate the
 Mycobacterium leprae."
 BASE COUNT 9493 a 13528 c 11679 g 8223 t
 ORIGIN

Query Match 62.3%; Score 21.8; DB 1; Length 42923;
 Best Local Similarity 78.8%; Pred. No. 1.4e+02;
 Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 gctggcgccctccggcgatcgaggagccca 34
 |||||
 Db 17290 GCTGGCGCGCCACCCCGGCACATCGCAAGTCCA 17258

RESULT 6
 STMTLP/c STMTLP 2188 bp DNA BCT 07-FEB-1999
 LOCUS Streptomyces erythraeus gene for trypsin-like protease, complete
 DEFINITION cds.
 NID
 ACCESSION D30760

NID 9493712
 VERSION D30760.1 GI:493712
 KEYWORDS trypsin-like protease.
 SOURCE Streptomyces erythraeus DNA.
 ORGANISM Saccharopolyspora erythraea
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 Actinomycetales; Pseudonocardiales; Pseudonocardaceae;
 Saccharopolyspora.
 1. (bases 1 to 2188)
 Norioka, S.
 Direct Submission
 Submitted (18-MAY-1994) to the DDBJ/EMBL/GenBank databases. Shigem
 Norioka, University of Osaka, Institute for protein research; 3-2
 Yamadaoka, Suita, Osaka 565, Japan (Tel:06-879-8618,
 Fax:06-876-2533)
 2. (bases 1 to 2188)
 Norioka, S.
 Unpublished (1996)
 3. (bases 1 to 2188)
 Nagamine-Matsuka, Y., Norioka, S. and Sakiyama, F.
 Molecular cloning, nucleotide sequence, and expression of the gene
 encoding a trypsin-like protease from Streptomyces erythraeus
 J. Biochem. 118 (2), 338-346 (1995)
 JOURNAL 96064153
 MEDLINE
 COMMENT Submitted (18-May-1994) to DDBJ by:
 Shigem Norioka
 Institute for protein research
 University of Osaka
 3-2 Yamadaoka
 Suita, Osaka 565
 Japan
 Phone: 06-879-8618
 Fax: 06-876-2533.
 Location/Qualifiers
 1. 2188
 /organism="Saccharopolyspora erythraea"
 /db_xref="taxon:1836"
 1049. 1867
 /codon_start=1
 /product="trypsin-like protease"
 /protein_id="BA06423.1"
 /db_xref="PID:d1006993"
 /db_xref="PID:g871932"
 /db_xref="GI:871932"
 /translation="MIRGSRRLAGTVAVLSAFAASVANATPPSPDDLTFFV
 GGEDANVDHPFTVALVTPDQCFQCGTLPAPNKVTAHCTVGSQPADINVSGRTV
 MSSNEGVSKVTNWVPEYODAAKGFDSVLTLEAPVKEAPIELAKADDAGYAPDTA
 ATILGWNTSEGQOAHLKATVPVNSDDTKQAYGEYTPDMVCGVPEGGVDTQC
 GDSCGPMVANNKLGIVTSWEGCARPGKPGVIARVGYDYVLMQINAGAVSAR"
 BASE COUNT 311 a 724 c 788 g 365 t
 ORIGIN
 5 ggcgcgcctccggcgatcgaggagccac 35
 ||||| ||||| ||||| ||||| |||||
 Db 509 GGAGCGCACCCGCGAGCGGCGCGCAC 479
 Query Match 61.1%; Score 21.4; DB 1; Length 2188;
 Best Local Similarity 80.6%; Pred. No. 3.8e+02;
 Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 FEATURES
 source
 CDS
 1. 2188
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="3 (human)"
 /cell_line="mouse/human"

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Homnidae; Homo.
 1. (bases 1 to 239)
 Zabarovskiy, E., Kashuba, V., Pettersson, B., Petrov, N., Zakhar'yev, V.,
 Gizatullin, R., Lebedeva, T., Bannikov, V., Erlandsson, R., Uhlen, M.,
 Kisselev, L. and Klein, G.
 Shot-gun sequencing strategy for long range genome mapping: first
 results
 Unpublished
 2. (bases 1 to 239)
 Zabarovskiy, E.
 Direct Submission
 Submitted (01-APR-1993) Zabarovskiy E., Karolinska Institute, Tumor
 Biology, S-104 01 Stockholm, Sweden
 Location/Qualifiers
 1. 239
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="3"
 /germline
 /clone="NL2273D"
 /cell_line="MCH903.1"
 /clone_lib="NL2"
 BASE COUNT 54 a 75 c 52 g 56 t 2 others
 ORIGIN
 5 ggcgcgcctccggcgatcgaggagccac 35
 ||||| ||||| ||||| ||||| |||||
 Db 86 GACGAGCTCCCGCGCGGCGGAGTCCCC 56
 RESULT 8
 HSNL2273D/c HSNL2273D 239 bp DNA PRI 01-JUL-1996
 LOCUS H.sapiens genomic DNA (chromosome 3; clone NL2273D).
 DEFINITION X87522
 ACCESSION G1418872
 NID X87522.1 GI:1418872
 VERSION X87522.1
 KEYWORDS human.
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Homnidae; Homo.
 1. (bases 1 to 239)
 Zabarovskiy, E.R.
 Unpublished
 2. (bases 1 to 239)
 Zabarovskiy, E.R.
 Direct Submission
 Submitted (03-MAY-1995) zabarovskiy E.R., Microbiology and
 Tumorbiology Center, Karolinska Institute, P.O. Box 280, Stockholm,
 S-171 77, SWEDEN
 Location/Qualifiers
 1. 239
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="3 (human)"
 /cell_line="mouse/human"

/clone_lib="Noti linking library"
 /clone="NL2273D"
 /note="genomic DNA surrounding NotI sites"
 BASE COUNT 54 a 75 c 52 g 56 t 2 others
 ORIGIN
 5 ggcgcgcctccggcgatcgaggagccac 35
 ||||| ||||| ||||| ||||| |||||
 Db 509 GGAGCGCACCCGCGAGCGGCGCGCAC 479
 Query Match 61.1%; Score 21.4; DB 10; Length 239;
 Best Local Similarity 80.6%; Pred. No. 6.8e+02;
 Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 ggcgcctccggcgagatcgagccac 35
 Db 86 GACGAGCCTCCCGCGGCTGGGAGTCCCC 56

RESULT 9 HS327J16/c LOCUS DEFINITION

HS327J16 111746 bp DNA PRI 15-JAN-1999
 Human DNA sequence from clone 327J16 on chromosome 22q12.3-13.2.
 Contains three novel genes: the human ortholog of mouse outer arm
 Dynein light chain 4, the human ortholog of rat Neuronal Pentraxin
 Receptor and a novel member of the CHROMOBOX protein genes
 family. Contains ESTs, STSS, a GSS and putative Cpg islands,
 complete sequence.

ACCESSION

NID AL008583
 VERSION 94160195
 KEYWORDS HTG; CHROMOBOX; Cpg Island; Neuronal Pentraxin Receptor; outer arm

SOURCE

ORGANISM human.
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 111746)
 TITLE Lloyd, D.
 JOURNAL Direct Submission

COMMENT

Submitted (28-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequests@sanger.ac.uk
 On Jan 16, 1999 this sequence version replaced gi:3892846.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 IMPORTANT: This sequence is not the entire insert of clone 327J16.
 It may be shorter because we only sequence overlapping sections
 once, or longer because we arrange for a small overlap between
 neighbouring submissions.
 The true left end of clone 150C2 (AL022318) is at 111647 in this
 sequence. The true right end of clone 779B17 (AL021806) is at 50467
 in this sequence.
 This sequence has been finished according to sequence map criteria
 as follows. An attempt is made to resolve all sequencing problems,
 such as compressions and repeats, but not necessarily within known
 annotated human repeat sequence elements (e.g. Alu). Where the
 sequence is ambiguous, there is an annotation using the 'unsure'
 feature key.

This sequence was generated from part of bacterial clone contigs of
 human chromosome 22, constructed by the Sanger Centre Chromosome 22
 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr22>
 327J16 is from the library RPC13 constructed at the Roswell Park
 Cancer Institute by the group of Pieter de Jong. For further
 details see <http://bacpac.med.buffalo.edu/VECTOR: pcypac2>.

FEATURES

Source

1. 111746
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="22"
 /clone="327J16"
 /map="q12.3-13.2"
 /clone_lib="RPC13"

repeat_region

149..325
 /note="MIR repeat: matches 8..184 of consensus"

repeat_region

549..860
 /note="AluX repeat: matches 1..312 of consensus"

repeat_region

875..1158
 /note="71 copies 4 mer tcca 82% conserved"

repeat_region

885..1142
 /note="129 copies 2 mer ca 58% conserved"

repeat_region

1240..1323
 /note="21 copies 4 mer tcca 82% conserved"

repeat_region

1332..1428
 /note="L2 repeat: matches 2615..2709 of consensus"

repeat_region

2109..2162
 /note="MIR repeat: matches 90..144 of consensus"

repeat_region

2240..2347
 /note="MIR repeat: matches 123..231 of consensus"

repeat_region

3395..3565
 /note="MIR repeat: matches 3..181 of consensus"

repeat_region

3819..3897
 /note="L2 repeat: matches 2447..2528 of consensus"

repeat_region

4507..4583
 /note="MIR repeat: matches 103..182 of consensus"

repeat_region

5473..5697
 /note="L2 repeat: matches 2486..2709 of consensus"

repeat_region

complement(join(5961..7066,8379..8462,10116..10323,
 21521..21608))

repeat_region

complement(join(5961..7066,8379..8462,10116..10323,
 21521..21608))

/gene="dj327J16.1"
 /note="match: CDNA AB010031; match: ESTs AA829582 AA675540
 AA270574 A112433 AA260435 AA007825 AA796378 AA881606
 R11814 AA394030 H14163 W69844 D31381 AA348039 AA877964
 AA322956 H55197 AA349185 AA895042 AA431647 AA278275
 AA039963 N42713 AA076578 T48120 W01618 A1182462 A1084123
 C85782 AA039935 AA935522 AA431283 AA076579 AA435541
 AA625556 AA427946 A1208576 A1222283 A1146263 AA725572
 N32499 A1240913 A1074275 AA279050 D81033 D61302 D60688
 D60515 D60397 D80885 D60658 AA431647 D81455 D80477"

/evidence="not experimental"
 /product="dj327J16.1 (human ortholog of mouse outer arm
 Dynein light chain 4)"

complement(5961..21608)
 /gene="dj327J16.1"

5961..6207
 /gene="dj327J16.1"

/note="match: STS G14738"
 complement(5961)

/gene="dj327J16.1"
 complement(join(6902..7066,8379..8462,10116..10184))

/note="match: proteins O54793 O44229"
 /codon_start=1

/evidence="not experimental"
 /product="dj327J16.1 (human ortholog of mouse outer arm
 Dynein light chain 4)"

/protein_id="CAA15429.1"
 /db_xref="PID:el370730"

/db_xref="PID:g4160196"
 /db_xref="GI:4160196"

/translation="MGTEGKKDEADYKRLQTFPLVRHSDMPPEMRYETMELCVTACE
 KFSNNESAAMKIMETMDKKFGSSWHVIGEGFGEITHEVKNLLLYFGGTLAVCVW
 KCS"

/note="MIR repeat: matches 22..241 of consensus"
 7858..7879

/note="L2 repeat: matches 2677..2707 of consensus"
 7980..8010

8825..9949
 /note="L2 repeat: matches 1478..2710 of consensus"

11159..11292
 /note="MIR repeat: matches 111..250 of consensus"

11253..11298
 /note="L2 repeat: matches 2653..2698 of consensus"

11654..11835
 /note="MIR repeat: matches 4..210 of consensus"

11960..12265
 /note="Alu repeat: matches 1..303 of consensus"

13157..13249
 /note="MIR repeat: matches 66..165 of consensus"

13730..14041
 /note="AluX repeat: matches 1..312 of consensus"

14570..14681
 /note="MIR repeat: matches 3..117 of consensus"

14682..14993

```

/Note="AluSq repeat: matches 2. .313 of consensus"
1494. .15027
/Note="MIR repeat: matches 116. .149 of consensus"
15248. .15431
/Note="MIR repeat: matches 21. .207 of consensus"
16498. .16566
/Note="L2 repeat: matches 2678. .2747 of consensus"
16513. .16720
/Note="MIR repeat: matches 24. .249 of consensus"
16721. .17028
/Note="AluJb repeat: matches 1. .298 of consensus"
17067. .17413
/Note="L2 repeat: matches 2289. .2620 of consensus"
17484. .17603
/Note="FLAM_C repeat: matches 2. .124 of consensus"
17889. .18022
/Note="L2 repeat: matches 1739. .1875 of consensus"
18098. .18338
/Note="Tigger3b repeat: matches 992. .1231 of consensus"
18339. .18648
/Note="AluX repeat: matches 1. .311 of consensus"
18649. .18795
/Note="Tigger3b repeat: matches 847. .992 of consensus"
18796. .19144
/Note="AluSp repeat: matches 1. .312 of consensus"
19147. .19457
/Note="AluX repeat: matches 1. .297 of consensus"
19458. .19722
/Note="Tigger3b repeat: matches 584. .847 of consensus"
19723. .20036
/Note="AluSq repeat: matches 1. .313 of consensus"
20037. .20604
/Note="Tigger3b repeat: matches 1. .584 of consensus"
20879. .21776
/Note="match: CpG island clones 279875 279876"
21060. .21158
/Note="MIR repeat: matches 38. .146 of consensus"
21949. .22069
/Note="MIR repeat: matches 89. .222 of consensus"
22390. .22986
/Note="LTR repeat: matches 1. .550 of consensus"
22988. .23418
/Note="L2 repeat: matches 1725. .2177 of consensus"
23419. .23559
/Note="LTR repeat: matches 550. .691 of consensus"
23560. .23681
/Note="L2 repeat: matches 2555. .2682 of consensus"
24316. .24509
/Note="L2 repeat: matches 1215. .1412 of consensus"
24671. .24769
/Note="L2 repeat: matches 1440. .1555 of consensus"
24770. .25095
/Note="AluYa5 repeat: matches 1. .311 of consensus"
25096. .25148
/Note="L2 repeat: matches 1555. .1603 of consensus"
25356. .26441
/Note="L2 repeat: matches 1618. .2707 of consensus"
26599. .26729
/Note="MLTJ repeat: matches 356. .499 of consensus"
26851. .27002
/Note="MLTJ repeat: matches 25. .182 of consensus"
27373. .27528

```

Query Match 60.6%; Score 21.2; DB 9; Length 111746;
 Best Local Similarity 76.5%; Pred. No. 1.6e+02;
 Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 gctgcgcgcctcccgccgagtcgggagccac 35
 ||| ||||| ||||| ||||| ||||| |||||
 Db 71360 GCCGCGCGCTCGCGGGGCTCGGCGCCCC 71327

RESULT 10

```

HS294778
LOCUS HS294778 315 bp DNA PRI 02-DEC-1997
DEFINITION H.sapiens genomic DNA fragment (clone NL1A177R).
ACCESSION Z94778
NID 92661883
VERSION Z94778.1 GI:2661883
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 315)
AUTHORS Gizatullin,R.Z., Kashuba,V.I., Protopopov,A.I. and Zabarovsky,E.R.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 315)
AUTHORS Zabarovsky,E.R.
TITLE Direct Submission
JOURNAL Submitted (18-APR-1997) Zabarovsky E.R., Karolinska Institute,
Microbiology and Tumorbiology Center, P.O. Box 280, Stockholm,
S-171 77, Sweden.
FEATURES
source
1..315
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/clone="NL1A177R"
/clone_lib="NL1 NotI linking library"
/lab_host="mouse/human microcell hybrid MCH903.1"
misc_feature
1..315
/Note="sequence surrounding NotI site"
BASE COUNT 46 a 106 c 127 g 36 t
ORIGIN

Query Match 60.6%; Score 21.2; DB 10; Length 315;
Best Local Similarity 76.5%; Pred. No. 7.3e+02;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 gctgcgcgcctcccgccgagtcgggagccac 35
||| ||||| ||||| ||||| ||||| |||||
Db 133 GCAGCGCGACCCCGCGGGGCTCGGAGCCAC 166

RESULT 11
HSDNASIAO/c
LOCUS HSDNASIAO 348 bp DNA PRI 01-JAN-1995
DEFINITION H.sapiens DNA sequence.
ACCESSION Z22459
NID 9608928
VERSION Z22459.1 GI:608928
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 348)
AUTHORS Zabarovsky,E., Kashuba,V., Pettersson,B., Petrov,N., Zakhar'yev,V.,
Gizatullin,R., Lebedeva,T., Bannikov,V., Erlandsson,R., Uhlen,M.,
Kisselev,L. and Klein,G.
TITLE Shot-gun sequencing strategy for long range genome mapping: first
results
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Zabarovsky,E.
TITLE Direct Submission
JOURNAL Submitted (01-APR-1993) Zabarovsky E., Karolinska Institute, Tumor
Biology, S-104 01 Stockholm, Sweden
FEATURES
source
1..348
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="chromosome.3"
/germline

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/clone="NLMP238D"
/cell_line="MCH903.1"
/clone_lib="NLM"
BASE COUNT 29 a 137 c 155 g 25 t 2 others
ORIGIN

Query Match 60.0%; Score 21; DB 10; Length 348;
Best Local Similarity 77.4%; Pred. No. 8.2e+02;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 ggcgcgcctccggcgagtcgggagccac 35
||||| ||||| ||||| ||||| |||||
Db 113 GCGCGGCTGCTGGCGGCGCGCGCCAC 83

RESULT 12
PFPOQABCF/c
LOCUS PFPQABCF 5137 bp DNA BCT 19-MAR-1996
DEFINITION P. fluorescens pqqf, pqaA, pqqB, pqqC genes.
ACCESSION X87299
X87299
NID 929799
VERSION X87299.1 GI:929799
KEYWORDS pqaA gene; pqqB gene; pqqC gene; pqqf gene; pyrroloquinoline
quinone biosynthesis.
SOURCE Pseudomonas fluorescens.
ORGANISM Pseudomonas fluorescens.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
Pseudomonas.

REFERENCE 1 (bases 1 to 5137)
AUTHORS Schnider U., Keel C., Voisard C., Defago C. and Haas D.
TITLE Tn5-directed cloning of pqq genes from Pseudomonas fluorescens
CHAO: mutational inactivation of the genes results in
overproduction of the antibiotic pyoluteorin
Appl. Environ. Microbiol. 61 (11), 3856-3864 (1995)
96064397
REFERENCE 2 (bases 1 to 5137)
AUTHORS Schnider U.
TITLE Direct Submission
JOURNAL Submitted (18-MAY-1995) U. Schnider, Laboratoire de Biologie
MICROBIENNE, Batiment de BIOLOGIE, UNIVERSITE DE LAUSANNE, CH- 1015
Lausanne-Dorigny, SWITZERLAND
LOCATION/Qualifiers
1. 5137
/organism="Pseudomonas fluorescens"
/strain="CHAO"
/db_xref="taxon:294"
CDS <1..350
/note="unidentified ORF1"
/codon_start=3
/transl_table=11
/protein_id="CAA60728.1"
/db_xref="PID:g929800"
/db_xref="GI:929800"
/db_xref="SPTREMBL:Q51807"
/translation="IYPKVDIASRIIGDPTVSWEADPHFGLGKALPGHYRNYQRM
YAHFMQDMPEAQEGIFAGDVSTPAWVEGAQVTSLSNAVGMKHFEGGATHAENPG
DVFHEIGPIALAD"
399..1256
/note="unidentified ORF2"
/codon_start=1
/transl_table=11
/protein_id="CAA60729.1"
/db_xref="PID:g929801"
/db_xref="GI:929801"
/db_xref="SWISS-PROT:P55176"
/translation="MSVEPATATVAGLSVSGVKTRVLYQCPRPILDVAGNIQRLH
QVAMEADADLVLPFELSGYNTGLEAVGALAEQDPSAORIAAQAAGTALVYG
YPERVDQIYNVQLIDAQQRCLNRYKTHFGDLDSHMFSGEDDFELVELDGWKL
GFLICDIEFFENARRALAGELIIVPTANMIPDFVADVITIRAFENQYVAYAN
YCGHEQIRYCGQSSIAAPDGSRIALAGLDEALIIGTLDQLMGESRALNRYLSRRP
ELYDDLKSR"
1276..3765
gene

/gene="pqqf"
1276..3765
/gene="pqqf"
/codon_start=1
/transl_table=11
/product="pyrroloquinoline quinone F biosynthesis"
/protein_id="CAA60730.1"
/db_xref="PID:g929802"
/db_xref="GI:929802"
/db_xref="SWISS-PROT:P55174"
/translation="MSASLFWKSCPRITILCPHWRQORLVRSLRHAPHKRCATIL
RYAGSHDVLAWPCLAHLEHLLFLGTERPEVOGLMAYVRAOGGOLNARTCERATL
FFELPASFAGGLERLCMLAQPRMSLEDQHREREVLHAEFIAMSRDATAPQRFALF
DGLHAAHFRAPFAGNRYSNLNPNNAFQALQOQFHREYIQAQWLSLAGPQPLELR
ALAEYRGSLPSGQHLQEQATPALMTGNQTYQLSGQRLDLFLFALERLPAGATAVD
FLCTWLQSAKPGGLLAELQQRQLASHLAKTILYEFAGALLHLEFLTSVAASAPVQ
RELTWELGFSQAQDAPLREEYVLLQORQIEVASALELSRRSRQADGIDESGLA
ALKOYLKOLQPAQVEHSHDWELPPANFLRSTIEAPRAGLIRGOTSAHRGLRTFAQD
RSRGRKSSALFSQALPADPSGSLTILWQLASAPMGLHARLSLRLATLDDARQA
GVELLFTSCGDKMLKLHGLSPMPAFVLLQALKLRPAESWQQAQSYNAEAPLLTI
ROLLKAFSEOPQDPSAPQDPPEALQALWASARWDGLGLALPAALQALSRILQCPFY
ADATLCRPVAGTQGWNLPGSAGEHALLLPYVPSASLADENARWLGQLCQPFY
ORLRYELOLGYGVFSVVRQNRGTGLFGVQSPGATVTEILQIAQLFHLPEQLQAL
DPSNDDQQAALQALQALPDLDOAMELLWQAKLAGHSSDYLPLQLOGCIEALTIPAIV
IQAKQLREAGGCSALANRCPGTFWQVAE"
3877..3996
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3877..3996
/gene="pqaA"
/codon_start=1
/transl_table=11
/product="pyrroloquinoline quinone A biosynthesis"
/protein_id="CAA60731.1"
/db_xref="PID:g929803"
/db_xref="GI:929803"
/db_xref="SWISS-PROT:P55171"
/translation="MIRQPSHPQRSNFWTWSKPATYDLRIGFEVMTYFASR"
3922..3996
/gene="alternative pqaA"
3922..3996
/gene="alternative pqaA"
/codon_start=1
/transl_table=11
/product="pyrroloquinoline quinone A biosynthesis"
/protein_id="CAA60732.1"
/db_xref="PID:g929804"
/db_xref="GI:929804"
/db_xref="SWISS-PROT:P55171"
/translation="MTWSRPAYTDLRIGFEVMTYFASR"
4101..5012
/gene="pqqB"
4101..5012
/gene="pqqB"
/codon_start=1
/transl_table=11
/product="pyrroloquinoline quinone B biosynthesis"
/protein_id="CAA60733.1"
/db_xref="PID:g929805"
/db_xref="GI:929805"
/db_xref="SWISS-PROT:P55172"
/translation="MFVILGSAGGFPQWNCNVCNACGRGSLRAQARTQSSIAL
SDDGVNVLNCSFDIRAQLFAPQMPQGRALRDIGIGAILMDSQIARTQGLLSLRE
GCPQVWCTDMWHEDISTGFLPKMLSHWNGLSWNRIELDQSFSPACPNLRFPLP
LRSAAAPPYSPHRFDHPGDNIGLIVELRSGGLFYAPGLKVDAPLLEMAASDVLL
VDGLTWEDEMQRGVCRTGTGREGHLAQNGPGCMLEVLQPLRQRKVLHINTNTPI
LDSDSRAELVLRKVEVADGMSIEL"
5105..5137
/gene="pqqC"
5105..5137
/gene="pqqC"
/codon_start=1
/transl_table=11
/product="pyrroloquinoline quinone C biosynthesis"

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/protein_id="CAA60734.1"
/db_xref="PID:9929806"
/db_xref="GI:929806"
/db_xref="SWISS-PROT:P551173"
/translation="MTDTPLSAEF"
BASE COUNT      928 a 1764 c 1545 g 900 t
ORIGIN

Query Match      58.9%; Score 20.6; DB 1; Length 5137;
Best Local Similarity 74.3%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 agctggcgccctcccgggcgatcgaggagccac 35
    ||||| | ||||| ||| ||||| |||||
Db 4834 AGGTGGCCCATTCGCGCGGTACGGTGCCAC 4800

RESULT 13
SC6G4/c
LOCUS      SC6G4      41055 bp      DNA      BCT      20-AUG-1998
DEFINITION Streptomyces coelicolor cosmid 6G4.
ACCESSION  AL031317
VERSION     93449234
KEYWORDS    AL031317.1 GI:3449234
            10 kb chaperonin; 30S ribosomal protein S11; 30S ribosomal protein
            S13; 30S ribosomal protein S9; 50S ribosomal protein L13; 50S
            ribosomal protein L17; 50S ribosomal protein L36; 60 kd chaperonin;
            acetyltransferase; acpS; adenylate kinase; adk; alanine racemase;
            alr; coaK; cpn10; cpn60; dehydrogenase; DNA-directed RNA polymerase
            alpha chain; gcp; glms; glucosamine-6-phosphate
            aminotransferase; groEL1; groES; holo-(acyl-carrier protein)
            synthase; InfA; lipase; map; methionine aminopeptidase;
            O-sialoglycoprotein endopeptidase; pantothenate kinase;
            phospho-sugar mutase; pseudouridyate synthase; rplM; rplQ; rpnJ;
            rpoA; rpl; rpsK; rpsM; translatiional initiation factor IF1; trua;
            two-component regulator.
SOURCE      Streptomyces coelicolor.
ORGANISM    Streptomyces coelicolor
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE   1 (bases 1 to 41055)
AUTHORS     Saunders,D. and Harris,D.
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 41055)
AUTHORS     Parkhill,J., Barrell,B.G. and Rajandream,M.A.
JOURNAL     Direct Submission
            Submitted (19-AUG-1998) Streptomyces coelicolor sequencing project,
            Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
            CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
            David A. Hopwood, [3] John Innes Centre, Norwich Research Park,,
            Colney, Norwich, Norfolk NR4 7UH, UK
            3 (bases 1 to 41055)
            Redenbach,M., Kieser,H.M., Denapaita,D., Eichner,A., Cullum,J.,
            Kinashi,H. and Hopwood,D.A.
            A set of ordered cosmids and a detailed genetic and physical map
            for the 8 Mb Streptomyces coelicolor A3(2) chromosome
            Mol. Microbiol. 21 (1), 77-96 (1996)
            97000351
COMMENT     Notes:
            Streptomyces coelicolor sequencing at The Sanger Centre is funded
            by the BBSRC.
            Details of S. coelicolor sequencing at the Sanger Centre are
            available on the World Wide Web.
            (URL: http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are
            numbered using the following system eg SC787.01c. SC (S.
            coelicolor), 787 (cosmid name), .01 (first CDS), c (complementary
            strand).
            The more significant matches with motifs in the PROSITE database
            are also included but some of these may be fortuitous. The length
            in codons is given for each CDS.
            Usually the highest scoring match found by fasta -o is given for
            CDS which show significant similarity to other CDS in the database.

```

```

FEATURES             source
source              1..41055
                  /organism="Streptomyces coelicolor"
                  /strain="A3(2)"
                  /db_xref="taxon:1902"
                  /clone="cosmid 6G4"
                  /locus="98.4% match to SCSECYDNA X83011 S.coelicolor secY
                  locus DNA from 4547 to 6154"
misc_feature        1..1610
                  /note="98.4% match to SCSECYDNA X83011 S.coelicolor secY
                  locus DNA from 4547 to 6154"
gene               1..286
                  /gene="adk"
                  /gene="adk"
                  /note="SC6G4.01, adk, adenylate kinase, partial CDS, len:
                  >94 aa; almost identical to KAD-STRCO adenylate kinase (EC
                  2.7.4.3) (205 aa) and highly similar to many e.g.
                  KAD-BORPE adenylate kinase (EC 2.7.4.3)(218 aa), fasta
                  scores: opt: 253 z-score: 429.1 E(): 1.2e-16, 50.6%
                  identity in 85 aa overlap. Contains pfam match to entry
                  PF00406 adenylatekinase, Adenylate kinases, score 136.80,
                  E-value 3.2e-37"
                  /codon_start=2
                  /transl_table=11
                  /product="adenylate kinase"
                  /protein_id="CAA20379.1"
                  /db_xref="PID:el318447"
                  /db_xref="PID:G3449235"
                  /db_xref="GI:3449235"
                  /db_xref="SPTREMBL:O86771"
                  /translation="INGRVCNRPKHVHYTPPKKGVCDVCGGELYQRDDSEE
                  TVKRLEVHTVTEPIIDYKSGQLVATTAATGPVDEVTRALEALKRQD"
                  2..208
                  /gene="adk"
                  /note="pfam match to entry PF00406 adenylatekinase,
                  Adenylate kinases, score 136.80, E-value 3.2e-37"
                  423..426
                  /note="possible RBS upstream of map"
                  438..1274
                  /gene="map"
                  438..1274
                  /gene="map"
                  /note="SC6G4.02, map, methionine aminopeptidase, len: 278
                  aa; identical to TR:O54208 (EMBL:X83011) methionine
                  aminopeptidase (278 aa) and highly similar to many
                  e.g.AMPM_BACSU methionine aminopeptidase (EC 3.4.11.18)
                  (248 aa), fasta scores: opt: 546 z-score: 922.2 E(): 0,
                  44.5% identity in 256 aa overlap. Also similar to S.
                  coelicolor map2 (E): 3.2e-33, 46.8% identity in 267 aa
                  overlap). Contains PS00680 Methionine aminopeptidase
                  subfamily 1 signature and pfam match to entry PF00557
                  pep_M24, metalloproteinase family M24, score 194.80,
                  E-value 1.4e-54"
                  /codon_start=1
                  /transl_table=11
                  /product="methionine aminopeptidase"

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The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at <http://www.nih.gov/jp/jun/cgi-bin/frameplot.pl>. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or att) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 6G4 lies between D31 and D63 in the AseI-D genomic restriction fragment.

FEATURES

source

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1..41055
/organism="Streptomyces coelicolor"
/strain="A3(2)"
/db_xref="taxon:1902"
/clone="cosmid 6G4"

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misc_feature

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1..1610
/note="98.4% match to SCSECYDNA X83011 S.coelicolor secY
locus DNA from 4547 to 6154"

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gene

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1..286
/gene="adk"
/gene="adk"

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CDS

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/note="SC6G4.01, adk, adenylate kinase, partial CDS, len:
>94 aa; almost identical to KAD-STRCO adenylate kinase (EC
2.7.4.3) (205 aa) and highly similar to many e.g.
KAD-BORPE adenylate kinase (EC 2.7.4.3)(218 aa), fasta
scores: opt: 253 z-score: 429.1 E(): 1.2e-16, 50.6%
identity in 85 aa overlap. Contains pfam match to entry
PF00406 adenylatekinase, Adenylate kinases, score 136.80,
E-value 3.2e-37"
/codon_start=2
/transl_table=11
/product="adenylate kinase"
/protein_id="CAA20379.1"
/db_xref="PID:el318447"
/db_xref="PID:G3449235"
/db_xref="GI:3449235"
/db_xref="SPTREMBL:O86771"
/translation="INGRVCNRPKHVHYTPPKKGVCDVCGGELYQRDDSEE
TVKRLEVHTVTEPIIDYKSGQLVATTAATGPVDEVTRALEALKRQD"

```

misc_feature

```

2..208
/gene="adk"

```

```

/note="pfam match to entry PF00406 adenylatekinase,
Adenylate kinases, score 136.80, E-value 3.2e-37"
423..426

```

```

/note="possible RBS upstream of map"

```

gene

```

438..1274
/gene="map"
438..1274

```

CDS

```

/gene="map"
/note="SC6G4.02, map, methionine aminopeptidase, len: 278
aa; identical to TR:O54208 (EMBL:X83011) methionine
aminopeptidase (278 aa) and highly similar to many
e.g.AMPM_BACSU methionine aminopeptidase (EC 3.4.11.18)
(248 aa), fasta scores: opt: 546 z-score: 922.2 E(): 0,
44.5% identity in 256 aa overlap. Also similar to S.
coelicolor map2 (E): 3.2e-33, 46.8% identity in 267 aa
overlap). Contains PS00680 Methionine aminopeptidase
subfamily 1 signature and pfam match to entry PF00557
pep_M24, metalloproteinase family M24, score 194.80,
E-value 1.4e-54"
/codon_start=1
/transl_table=11
/product="methionine aminopeptidase"

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/misc_feature
/protein_id="CAA20380.1"
/db_xref="PID:e1316448"
/db_xref="PID:g3449236"
/db_xref="GI:3449236"
/db_xref="SP:RMBL054208"
/translation="MVOIKRPEQIAKREAGLVAAIHAAATREAAVPGATTKDLDOVA
RKVLAAHDAKPNELGSGFPATICTSVNEVHGIPSDDDVVLKGDVVISDCGAILDG
WHGDAATFVSGHSPGLVELSVTEESWAGIAAKOGNRLVDVSRATETVIRQP
KPGGKGIIDYGGHIGTEMHMDPHLLNVDRRKGKPKLVPGFCLAIETPMVSLGT
PRTEVLPEDETVITTDGTSSHWEHSVALTEQGPLVLTSPDGCKAKLAELGITAAPDP
LA"
444..1196
/gene="map"
/notes="Pfam match to entry PF00557 pep_M24,
metallopeptidase family M24, score 194.80, E-value
1.4e-54"
954..1010
/gene="map"
/notes="PS00680 Methionine aminopeptidase subfamily 1
signature"
1405..1408
/notes="possible RBS upstream of Infa"
1416..1637
/gene="infa"
1416..1637
/gene="infa"
/notes="SC64.03, infa, translational initiation factor
IF1, len: 73 aa; identical to TR:054209 (EMBL:X83011)
translational initiation factor IF1 (fragment) (65 aa) and
highly similar to many e.g. IF1_BACSU translation
initiation factor IF-1 (71 aa), fasta scores; opt: 384
z-score: 792.5 E(): 0, 78.6% identity in 70 aa overlap.
Contains Pfam match to entry PF00575 S1, S1 RNA binding
motif, score 54.10, E-value 3.1e-12"
/codon_start=1
/transl_table=11
/product="translational initiation factor IF1"
/protein_id="CAA20381.1"
/db_xref="PID:e1316449"
/db_xref="PID:g3449237"
/db_xref="GI:3449237"
/translation="MAKOGAIEGTVVESLPNMPKVELQNGHVLAHISGMKRVH
YIRLPDRVVVELSPYDLTRGIVRYK"
1422..1634
/gene="infa"
/notes="Pfam match to entry PF00575 S1, S1 RNA binding
motif, score 54.10, E-value 3.1e-12"
1690..1693
/notes="possible RBS upstream of rpmj"
1706..1816
/gene="rpmj"
/notes="Pfam match to entry PF00444 L36, Ribosomal protein
L36, score 70.40, E-value 3.1e-22"
1706..1819
/gene="rpmj"
1706..1819
/gene="rpmj"
/notes="SC64.04, rpmj, 50S ribosomal protein L36, len: 37
aa; highly similar to many e.g. RL36_BACST 50S ribosomal
protein L36 (37 aa), fasta scores; opt: 225 z-score: 380.1
E(): 6.6e-14, 78.4% identity in 37 aa overlap. Contains
PS00828 Ribosomal protein L36 signature and Pfam match to
entry PF00444 L36, Ribosomal protein L36, score 70.40,
E-value 3.1e-22"
/codon_start=1
/transl_table=11
/product="50S ribosomal protein L36"
/protein_id="CAA20382.1"
/db_xref="PID:e1316450"
/db_xref="PID:g3449238"
/db_xref="GI:3449238"
/db_xref="SP:RMBL086772"
/translation="MKVPSVKKICKRCVIRRRGVNVCIDNPRHKORQS"

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```

misc_feature 1736..1813
Query Match 58.3%; Score 20.4; DB 1; Length 41055;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 gcgcgcctcccgccggcgatcgaggagccac 35
||||| ||||||| ||||| |||
Db 11527 GCGCCGCCGCGCGGAGCGGCCGCC 11498

RESULT 14
D86087S01/c
LOCUS D86087S01 1506 bp DNA PRI 07-FEB-1999
DEFINITION Human DNA for prostaglandin E receptor EP3 subtype, exon 1.
ACCESSION D86087
NID 92114177
VERSION D86087.1 GI:2114177
KEYWORDS prostaglandin E receptor EP3 subtype.
SEGMENT 1 of 10
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1506)
AUTHORS Kotani, M.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-1996) to the DDBJ/EMBL/GenBank databases. Masato
Kotani, Kyoto University Graduate School of Medicine, Dept. of Med.
and Clin. Sci; 54 Shogoin-kawahara-cho, Kyoto, Kyoto 606, Japan
(fel:075-751-4285, fax:075-771-9452)
REFERENCE 2 (bases 1 to 1506)
AUTHORS Kotani, M., Tanaka, I., Ogawa, Y., Usui, T., Nakao, K. and Narumiya, S.
TITLE The human prostaglandin E receptor EP3 subtype gene
JOURNAL Unpublished (1996)
REFERENCE 3 (sites)
AUTHORS Kotani, M., Tanaka, I., Ogawa, Y., Usui, T., Tamura, N., Mori, K.,
Narumiya, S., Yoshimi, T. and Nakao, K.
TITLE Structural organization of the human prostaglandin EP3 receptor
subtype gene (PTGER3)
JOURNAL Genomics 40 (3), 425-434 (1997)
MEDLINE 97230456
FEATURES
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/db_xref="taxon:9606"
/chromosome="1"
/clone="LHEP1"
/clone_lib="LEMBL3"
GC_signal 361..591
5'UTR 310..315
exon 361..1488
intron 1489..1506
/standard_name="prostaglandin E receptor EP3 subtype gene"
BASE COUNT 216 a 531 c 478 g 281 t
ORIGIN
Query Match 58.3%; Score 20.4; DB 9; Length 1506;
Best Local Similarity 80.0%; Pred. No. 8.5e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 gcgcgcctcccgccggcgatcgaggagccac 35
||||| ||||||| ||||| |||
Db 186 GCCCTGCTCTCGCGGAGCGGCCGCCAC 157

RESULT 15

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HS333A15

LOCUS HS333A15 133221 bp DNA PRI 12-MAY-1999
 DEFINITION Human DNA sequence from clone 333A15 on chromosome 1p31.1-31.3,
 complete sequence.
 ACCESSION AL031429
 NID G4775605
 VERSION AL031429.11 GI:4775605
 KEYWORDS HTG; Cpg Island.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 133221)
 DIRECT SUBMISSION
 Submitted (12-MAY-1999) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk

COMMENT

On May 11, 1999 this sequence version replaced G1:4688871.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 EM: EMBL; SW: SWISSPROT; Tr: TREMBL
 This sequence is the entire insert of clone 333A15. This sequence
 has been finished according to sequence map criteria as follows. An
 attempt is made to resolve all sequencing problems, such as
 compressions and repeats, but not necessarily within known
 annotated human repeat sequence elements (e.g. Alu). Where the
 sequence is ambiguous, there is an annotation using the 'unsure'
 feature key.

This sequence was generated from part of bacterial clone contigs of
 human chromosome 1, constructed by the Sanger Centre Chromosome 1
 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr1>
 333A15 is from the library RCI13 constructed at the Roswell Park
 Cancer Institute by the group of Pieter de Jong. For further
 details see <http://bacpac.med.buffalo.edu/VECTOR:pcypac2>.

FEATURES

source

1.133221
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 /db_xref="taxon:9606"
 /chromosome="1"
 /clone="333A15"
 /map="p31.1-31.3"
 /clone_lib="RCI13"
 1.1067

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1319. .1373
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1376. .1642
 /note="AluX repeat: matches 1. .267 of consensus"

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1721. .1979
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2515. .3677
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3678. .4132
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4459. .4554
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4690. .4991
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5197. .5234
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5201. .5232
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5235. .5274
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 consensus"

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8760. .9114
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9153. .9222
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9224. .9283
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9228. .9283
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9374. .9530
 /note="L2 repeat: matches 2550. .2710 of consensus"

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11999. .12032
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11999. .12034
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12473. .12626
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12732. .12775
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13731. .13821
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14867. .15211
 /note="THE1A repeat: matches 3. .352 of consensus"

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15218. .16792
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 consensus"

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16793. .17146
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17835. .18314
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18740. .18956
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19354. .19584
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20167. .20252
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21372. .21487
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22488. .22559
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22653. .22796
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23312. .23485
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25760. .25918
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26081. .26160
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28026. .28557
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30092. .30149
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repeat_region

30835. .30989
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repeat_region

31453. .31661

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33066. .33334
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33898. .35690
repeat_region /note="L1MA6 repeat: matches 4491. .6300 of consensus"
35691. .35998
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35999. .36035
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36174. .36607
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37248. .37439
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37472. .37593
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38364. .38554
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38765. .39132
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consensus"
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42840. .43411
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46225. .46394
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46944. .46997
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Query Match      58.3%; Score 20.4; DB 10; Length 133221;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 124320 GCCCTGCTCCTGCGCGGACCGGCCAC 124349

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Search completed: September 28, 1999, 16:46:27
Job time: 7374 sec

RESULT 5
US-08-442-282-4/c
; Sequence 4, Application US/08442382
; Patent No. 5760204
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira

RESULT 6

APPLICANT: Takaga, Satoshi
 APPLICANT: Murata, Yoshiyuki
 TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/757,390
 FILING DATE: 19910910
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 7005-030
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 8698864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1808 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: CDNA
US-07-757-390-2

Query Match 1.4%; Score 94.2; DB 1; Length 1808;
Best Local Similarity 80.8%; Pred. No. 5.7e-16;
Matches 122; Conservative 0; Mismatches 28; Indels 1; Gaps 1;
QY 378 gtttggttgagttttgtttatttagacagggctctctgtgtgtagtctgtgcttcc 437
DB 1808 GTTTGTTGTTGTTGTTGTTTTCGAGACAGGGTTTCTCTGTGTAGCTCTGGCTGTC-T 1750
QY 438 ggaactcactctgtagaccaggtggtccttgaaactcagaataacgcctgctgtgcttcc 497
DB 1749 GGAACCTCACTTTATAGACCAAGCTGGCTCGAAGCTCAGAAATCCCTCCGCTGTGTCATCC 1690
QY 498 caagtgccttagattaaagggtgcaactgccca 528
DB 1689 CAGGTGCTGGTATTAAAGCGAGCTCTACCA 1659

RESULT 11
US-07-757-390-15/C
Sequence 15, Application US/07757390
Patent No. 5453491
GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tomimaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,390
FILING DATE: 19910910
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1808 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 303...1547
US-07-757-390-15

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Best Local Similarity 80.8%; Pred. No. 5.7e-16;
Matches 122; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

QY 378 gtttggttgagttttgtttatttagacagggctctctgtgtgtagtctgtgcttcc 437
DB 1808 GTTTGTTGTTGTTGTTGTTTTCGAGACAGGGTTTCTCTGTGTAGCTCTGGCTGTC-T 1750
QY 438 ggaactcactctgtagaccaggtggtccttgaaactcagaataacgcctgctgtgcttcc 497
DB 1749 GGAACCTCACTTTATAGACCAAGCTGGCTCGAAGCTCAGAAATCCCTCCGCTGTGTCATCC 1690
QY 498 caagtgccttagattaaagggtgcaactgccca 528
DB 1689 CAGGTGCTGGTATTAAAGCGAGCTCTACCA 1659

RESULT 12
US-08-442-282-2/C
Sequence 2, Application US/08442282
Patent No. 5760204
GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tomimaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,282
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1808 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-442-282-2

Query Match 1.4%; Score 94.2; DB 3; Length 1808;
Best Local Similarity 80.8%; Pred. No. 5.7e-16;
Matches 122; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

QY 378 gtttggttgagttttgtttatttagacagggctctctgtgtgtagtctgtgcttcc 437
DB 1808 GTTTGTTGTTGTTGTTGTTTTCGAGACAGGGTTTCTCTGTGTAGCTCTGGCTGTC-T 1750
QY 438 ggaactcactctgtagaccaggtggtccttgaaactcagaataacgcctgctgtgcttcc 497
DB 1749 GGAACCTCACTTTATAGACCAAGCTGGCTCGAAGCTCAGAAATCCCTCCGCTGTGTCATCC 1690

Search completed: September 28, 1999, 16:41:07
Job time: 7053 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 28, 1999, 16:50:24 ; Search time 303.81 Seconds
(without alignments)
28.823 Million cell updates/sec

US-09-037-657-30
Title: 35
Perfect score: 1
Sequence: agctggcgccctcccgaggatcgggagccac 35

Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	35	100.0	35	1	V27146	Murine NR6.1 prime
2	20.2	57.7	1930	1	V27158	Unspliced murine N
3	20.2	57.7	1629	1	V27140	Novel haemopoietin
4	20.2	57.7	1673	1	V27141	Novel haemopoietin
5	20.2	57.7	1656	1	V41688	Nucleotide sequenc
6	20.2	57.7	1724	1	V70896	cDNA encoding rat
C 7	19.6	56.0	1496	1	T87165	UL49 homologue gen
8	19.6	56.0	2861	1	T64785	Human oxygen regul
9	19.2	54.9	6306	1	Q54841	Sequence encoding
10	19.2	54.9	6819	1	T77782	cDNA encoding GAL4
11	19.2	54.9	6579	1	T77783	cDNA encoding LexA
C 12	19	54.3	2271	1	Q62176	Human TLE-2 gene.
C 13	19	54.3	2271	1	Q45334	Human TLE-2 gene.
14	18.8	53.7	15079	1	Q91580	S. clavuligerus cl
C 15	18.8	53.7	3946	1	T93610	Mycobacterium tube
16	18.6	53.1	1578	1	Q61817	Open reading frame
17	18.6	53.1	2544	1	T67066	Human alpha3(IX) c
C 18	18.4	52.6	1700	1	Q45569	Sequence soyac and
C 19	18.2	52.0	1306	1	Q27827	Bovine TP (CDNA cl
C 20	18.2	52.0	1316	1	Q53210	Human cyclin D1 pr
21	18.2	52.0	2256	1	T32999	Chimaeric thermost
C 22	18.2	52.0	30001	1	T61016	Total DNA sequenc
C 23	18.2	52.0	4767	1	V21648	AAV4 genome. Adeno
C 24	18.2	52.0	2208	1	V21650	AAV4 VP1 capsid pr
C 25	18.2	52.0	1800	1	V21657	AAV4 VP2 coat prot
C 26	18.2	52.0	1617	1	V21658	AAV4 VP3 coat prot
27	18.2	52.0	11832	1	V27148	Nucleotide sequenc
28	18.2	52.0	3763	1	V58134	Human myosin I-cha
29	18.2	52.0	2933	1	V59665	Human secreted pro
C 30	18.2	52.0	3306	1	V80595	Kidney injury asso
C 31	18.2	52.0	925	1	V99229	DNA encoding an ac
C 32	18.2	52.0	30001	1	X05110	S. aureofaciens DN
C 33	18	51.4	2565	1	Q01810	Sequence encoding
C 34	18	51.4	2659	1	Q10164	Cyclomaltodextrin
35	18	51.4	1845	1	Q78162	dUTPase of bovine
36	18	51.4	290	1	Q73982	Cellulobiose gene fr
37	18	51.4	2369	1	V38669	Mus musculus SOCS6
C 38	17.8	50.9	4244	1	Q28889	PRADI. New cyclin
C 39	17.8	50.9	1325	1	Q31873	Cyclin D1 gene. Re
C 40	17.8	50.9	1317	1	Q31878	Cyclin D1 promoter
C 41	17.8	50.9	1325	1	Q53197	Human cyclin D1. N
C 42	17.8	50.9	3836	1	Q53997	Vitamin D hydroxyl
C 43	17.8	50.9	4221	1	Q64046	A253 derived bel-1

ALIGNMENTS

c	44	17.8	50.9	476	1	Q64047	bcl-1 probe G13b.
	45	17.8	50.9	573	1	T16631	Hepatitis C virus

RESULT 1

V27146	V27146 standard; DNA; 35 BP.
ID	V27146; AC
AD	29-SEP-1998 (first entry)
DT	Murine NR6.1 primer 5N.
DE	Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW	cell survival; therapeutic; neuronal proliferation; drug screening; ss;
KW	Mouse; PCR; primer; amplification.
KW	Synthetic.
OS	OS
OS	Mus sp.
PN	WO9811225-A2.
PN	19-MAR-1998.
PD	11-SEP-1997; G02479.
PF	11-SEP-1996; AU-002246.
PR	(AMRA-) AMRAD OPERATIONS PTY LTD.
PA	(DZTE/) DZIEGLEWSKA H E.
PI	Alexander W, Fabril L, Farley A, Hilton DJ, Kikuchi Y,
PI	Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
PI	Zhang J;
PI	WPI: 98-260970/23.
DR	New isolated haemopoietin receptor - used for developing products
PT	for modulating proliferation, differentiation and survival of cells,
PT	e.g. neuronal cells
PT	Claim 29(4); Page 54; 182pp; English.
PS	The primers V27146 and V27147 were used to amplify the mouse NR6.1 coding
CC	region. NR6.1 is a form of NR6 a novel Haemopoietin receptor (HR).
CC	Interaction between the novel HR and a ligand facilitates proliferation,
CC	differentiation and survival of a wide variety of cells. The HR and it's
CC	derivatives can be used for modulating the activity of the receptors e.g.
CC	to regulate development, maintenance or regeneration in an array of
CC	different cells and tissues in vitro and in vivo. They can be present in
CC	therapeutics used for modulating neuronal proliferation, differentiation
CC	and survival. The products can also be used for detection and diagnosis,
CC	e.g. for cancers or predisposition to cancers, or for drug screening.
CC	Sequence 35 BP; 14 C; 14 G; 3 T;
SQ	

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Query Match      100.0%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred: No. 0.00078;
Matches 35; Conservative 0; Mismatches 0; Indels
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Qy 1 agctggcgccctcccgccggatcgggagccac 35
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Db 1 AGCTGGCGCCCTCCGGCGGATCGGAGCCAC 35

RESULT 2

V27158	V27158 standard; DNA; 1930 BP.
ID	V27158; AC
AC	V27158; AC
DE	29-SEP-1998 (first entry)
DT	Unspliced murine NR6 nucleotide sequence.
DR	Endoproteinase Lys-C digestion of the
KW	Hemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW	cell survival; therapeutic; neuronal proliferation; drug screening; ss;
OS	Mouse.
OS	Mus sp.
PN	WO98111225-A2.
PD	19-MAR-1998.
PF	11-SEP-1997. G02479.
PF	11-SEP-1996; AU-002246.
PR	(AMRA-) AMRAD OPERATIONS PTY LTD.
PA	(DZIE-) DZIEGLEWSKA H E.
PI	Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI	Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
PI	Zhang J.

DR WPI: 98-260970/23.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PS Example 8: Page 99-100; 182pp; English.
CC NR6 is a novel haemopoietin receptor (HR). Interaction between the novel
CC HR and a ligand facilitates proliferation, differentiation and survival
CC of a wide variety of cells. The HR and its derivatives can be used for
CC modulating the activity of the receptors e.g. to regulate development,
CC maintenance or regeneration in an array of different cells and tissues in
CC vitro and in vivo. They can be present in therapeutics used for
CC modulating neuronal proliferation, differentiation and survival. The
CC products can also be used for detection and diagnosis, e.g. for cancers
CC or predisposition to cancers, or for drug screening.
SQ Sequence 1930 BP; 375 A; 623 C; 561 G; 371 T;

Query Match 57.7%; Score 20.2; DB 1; Length 1930;
Best Local Similarity 75.8%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 ctggcgccctcccgccggatcgaggccac 35
DB 218 CTCGGGGTGCCTCGGGCGGATCGGGAGCCAC 250
|||||

RESULT 3
V27140
ID V27140 standard; cDNA; 1629 BP.
AC V27140;
DE 29-SEP-1998 (first entry)
DE Novel haemopoietin receptor NR6.1 gene.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening; ss;
KW Mouse.
OS Mus sp.
FH Key
FT CDS
FT Location/Qualifiers
FT 113..1355
FT /*tag= a
FT /product= "Haemopoietin receptor NR6.1"
PN WO9811225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIE/) DZIEGLEWSKA H E.
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
PI Zhang J;
PI WPI: 98-260970/23.
PI P-PSDB: W55011.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PS Claim 4; Page 77-81; 182pp; English.
CC The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6.
CC Interaction between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and its
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SQ Sequence 1629 BP; 336 A; 541 C; 453 G; 299 T;

Query Match 57.7%; Score 20.2; DB 1; Length 1629;
Best Local Similarity 75.8%; Pred. No. 46;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 ctggcgccctcccgccggatcgaggccac 35
DB 218 CTCGGGGTGCCTCGGGCGGATCGGGAGCCAC 35
|||||

DB 217 CTCGGGGTGCCTCGGGCGGATCGGGAGCCAC 249
RESULT 4
V27141
ID V27141 standard; cDNA; 1673 BP.
AC V27141;
DE 29-SEP-1998 (first entry)
DE Novel haemopoietin receptor NR6.2 gene.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening; ss;
KW Mouse.
OS Mus sp.
FH Key
FT CDS
FT Location/Qualifiers
FT 1..1278
FT /*tag= a
FT /product= "Haemopoietin receptor NR6.2"
PN WO9811225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIE/) DZIEGLEWSKA H E.
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
PI Zhang J;
PI WPI: 98-260970/23.
PI P-PSDB: W55012.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PS Claim 5; Page 84-87; 182pp; English.
CC The haemopoietin receptor (HR) NR6.2 is a form of the novel HR NR6.
CC Interaction between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and its
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SQ Sequence 1673 BP; 344 A; 550 C; 474 G; 305 T;

Query Match 57.7%; Score 20.2; DB 1; Length 1673;
Best Local Similarity 75.8%; Pred. No. 46;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 ctggcgccctcccgccggatcgaggccac 35
DB 218 CTCGGGGTGCCTCGGGCGGATCGGGAGCCAC 250
|||||

RESULT 5
V41688
ID V41688 standard; cDNA; 1656 BP.
AC V41688;
DE 26-OCT-1998 (first entry)
DE Nucleotide sequence of the murine U4 gene.
KW Murine; U4 protein; haemopoietin receptor superfamily;
KW cell proliferation; immune response; antibody; cell differentiation;
KW autoimmune disease; cancer; allergy; ds.
OS Mus sp.
FH Key
FT CDS
FT Location/Qualifiers
FT 122..1399
FT /*tag= a
FT /product= "U4 protein"
PN WO9831811-A1.
PD 23-JUL-1998.
PF 15-JAN-1998; U00334.
PR 16-JAN-1997; US-784863.
PA (GENY) GENETICS INST INC.
PI Collins M, Donaldson DD, Neben T, Whitters M;

WPI; 98-414109/35.
P-PSDB; W59804.

New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response; for treating cancer and auto-immune disease

Claim 1; Pages 25-26; 39pp; English.

This is the nucleotide sequence encoding the murine U4 protein from the haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and as tissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases, cancer, and allergy).

Sequence 1656 BP; 318 A; 552 C; 478 G; 308 T;

Query Match 57.7%; Score 20.2; DB 1; Length 1656;
Best Local Similarity 75.8%; Pred. No. 46;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps

QY 3 cttgcgctcccggtcggatcgaggagcccac 35
||| | | |||||||||
Db 215 CTCGGGTCCTCGGGCGGATCGGAGCCAC 247

RESULT 6
V70896
ID V70896 standard; cDNA; 1724 BP.
DT 17-MAR-1999 (first entry)
DE cDNA encoding rat Zcytor5
KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
KW cardiac pathology; heart enlargement; Zcytor5 ligand; ss.
OS Rattus sp.
FT Key Location/Qualifiers
FT EDS 159..1436
FT /*tag= a
FT /product= zcytor5
FN W09849307-Al.
PD 05-NOV-1998.
PP 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PPA (ZYMO) ZYMOGENETICS INC.
PPA Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JW,
PPI Lok S, Presnell SR, Whitmore TE;
PPI WPI; 99-034662/03.
PDR P-PSDB; W70862.
PDR New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
PDR down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
PDR in blood
PPS Disclosure; Page 72-75; 55pp; English.
CCC The present sequence encodes a protein designated Zcytor5, which is
CCC a cytokinin-like receptor. Soluble Zcytor5 may be administered to
CCC down-regulate the effects of a growth and/or maintenance factor in
CCC thyroid, heart, and skeletal muscle for example to lessen the effect
CCC of cardiotrophin-1 on cardiac pathologies, so preventing heart
CCC enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the
CCC blood, and to discover other possible Zcytor5 ligands. A probe
CCC comprising Zcytor5 DNA or RNA can be used to determine the presence
CCC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
CCC anti-idiotypic antibody could be used to purify Zcytor5 and
CCC therapeutically to modify Zcytor5 ligand effects.
CCC Sequence 1724 BP; 350 A; 550 G; 324 T;

```

Query Match          54.9%; Score 19.2; DB 1; Length 6306;
Best Local Similarity 87.5%; Pred. No. 87;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

        6 gcgcgcctccgcggcgatcgaggga 29
        ||| ||||| ||||| ||| |||||
3459  GCGGCGCTCCCGGCTGAGCGGGA 3482

RESULT 10
T77782 standard; cDNA; 6819 BP.
T77782:
01-OCT-1997 (first entry)
cDNA encoding GAL4/HA/NUMA fusion protein.
NIP-1; NIP-2; NUMA; nuclear mitotic apparatus; NUMA interacting protein;
cell division; proliferation; antibody; Ab; detection;
malignant cell growth; ss.
Homo sapiens.
Key Location/Qualifiers
misc_feature 1..441
/*tag= a
/product= GAL4 DNA binding domain
misc_feature 442..522
/*tag= b
/product= hemagglutinin tag
mat_peptide 523..6819
/*tag= C
/product= Residues 18-2116 of NUMA

W09640917-41.
19-DEC-1996.
P-PSDB; W21731.
P-PSDB; W21731.
New nucleic acid encoding nuclear mitotic appts. interacting
proteins - useful for modulating cell division and proliferation and
in diagnosis
Claim 16; Page 28-36; 78pp; English.
The sequences given in T77782-83 encode fusion proteins which contain
NUMA (nuclear mitotic apparatus). The fusion proteins were used in
the identification of NUMA interacting proteins (NIP's) (see also
W21729-30). Compounds which interfere with the interaction of NUMA
with a known NIP are used to modulate cell division and/or proliferation.
Ab, raised conventionally using NIP-1 or -2 as immunogen, are used to
detect NIP (or their complexes) and to block their activity for
diagnostic or therapeutic use, e.g. to detect defective NUMA or NIP
which may be markers for aberrant (including malignant) cell growth
(which can also be detected by nucleic acid sequencing). Also where
malignancy is related to defects in NUMA or NIP, it can be treated by
administration of the appropriate functional protein.
Sequence 6819 BP; 1796 A; 1841 C; 2135 G; 1046 T;

Query Match          54.9%; Score 19.2; DB 1; Length 6819;
Best Local Similarity 87.5%; Pred. No. 87;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

        6 gcgcgcctccgcggcgatcgaggga 29
        ||| ||||| ||||| ||| |||||
3930  GCGGCGCTCCCGGCTGAGCGGGA 3953

RESULT 11
T77783
ID T77783 standard; cDNA; 6579 BP.
AC T77783;
DT 01-OCT-1997 (first entry)
DE cDNA encoding LexA/NUMA fusion protein.

```

KW NIP-1; NIP-2; NUMA; nuclear mitotic apparatus; NUMA interacting protein;
 KW cell division; proliferation; antibody; Ab; detection;
 KW malignant cell growth; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc_feature 1..261
 FT /tag= a
 FT /product= Lexa DNA binding domain
 FT misc_feature 262..283
 FT /tag= b
 FT /note= "Polylinker"
 FT mat_peptide 284..6579
 FT /tag= c
 FT /product= Residues 18-2116 of NUMA
 FT W09640917-A1.
 PN 19-DEC-1996.
 PD 07-JUN-1996; U09504.
 PE 07-JUN-1996; US-478408.
 PR (UYIA) UNIV YALE.
 PA McPherson SMG, Snyder MP;
 PI WPI: 97-077270/07.
 DR P-PSDB: W21732.
 PT New nucleic acid encoding nuclear mitotic appts. Interacting
 PT proteins - useful for modulating cell division and proliferation and
 PT in diagnosis
 PS Claim 16; Page 42-50; 78pp; English.
 CC The sequences given in T77782-83 encode fusion proteins which contain
 CC NUMA (nuclear mitotic apparatus). The fusion proteins were used in
 CC the identification of NUMA interacting proteins (NIP's) (see also
 CC W21729-30). Compounds which interfere with the interaction of NUMA
 CC with a known NIP are used to modulate cell division and/or proliferation.
 CC Ab, raised conventionally using NIP-1 or -2 as immunogen, are used to
 CC detect NIP (or their complexes) and to block their activity for
 CC diagnostic or therapeutic use, e.g. to detect defective NUMA or NIP
 CC which may be markers for aberrant (including malignant) cell growth
 CC (which can also be detected by nucleic acid sequencing). Also where
 CC malignancy is related to defects in NUMA or NIP, it can be treated by
 CC administration of the appropriate functional protein.
 CC Sequence 6579 BP; 1691 A; 1806 C; 2107 G; 975 T;
 SQ

Query Match 54.9%; Score 19.2; DB 1; Length 6579;
 Best Local Similarity 87.5%; Pred. No. 87;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 6 gcgcgcctccggcggtatcgga 29
 Db 3690 GCGGCGCTCCGCGGTGACGGGA 3713
 RESULT 12
 Q62176/c
 ID Q62176 standard; cDNA; 2271 BP.
 AC Q62176;
 DT 10-SEP-1994 (first entry)
 DE Human TLE-2 gene.
 KW TLE-2; transducin-like enhancer of split protein; differentiation;
 KW protein transport; cervix cancer; dysplasia; malignancy;
 KW ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc_feature 26..2257
 FT /tag= a
 FT W09408037-A.
 PN 14-APR-1994.
 PD 30-SEP-1993; U09333.
 PE 30-SEP-1992; US-955011.
 PR (MEDI-) MEDICAL RES COUNCIL.
 PA (UYIA) UNIV YALE.
 PI Artavanis-tsakonas S, Hill RE, Redhead NJ, Stifani S;
 DR WPI: 94-135597/16.
 DR P-PSDB: R51477.
 PT New human transducin-like enhancers of split protein - and

PT associated multi-protein complexes, chimeric proteins,
 PT antibodies, nucleic acid, etc., involved in nuclear-cytoplasmic
 PT protein transport
 PS Disclosure; Page 58-61; 112pp; English.
 CC The nucleotide and deduced aa sequences of human transducin-like
 CC enhancer of split proteins TLE-1 (Q62175, R51476), TLE-2 (Q62176,
 CC R51477), TLE-3 (Q62177, R51478) and TLE-4 (Q62178, R51479) were
 CC determined. The aa sequences were compared with that of Drosophila
 CC E(spl)m9/10 protein (R51481). Comparison of the WD-40 domains of
 CC these proteins defined the consensus residues shown in R51480. The
 CC Ccn motifs of the proteins were compared with those of the SV40 T
 CC antigen, human c-myc, human p53, human A-myb and dorsal proteins
 CC with respect to nuclear localization site, and casein-kinase II and
 CC cdc2-kinase phosphorylation sites (sequences R51482-96). TLE can be
 CC used to treat or diagnose (pre)neoplastic conditions, or
 CC to study cell differentiation.
 SQ Sequence 2271 BP; 437 A; 751 C; 672 G; 411 T;
 Query Match 54.3%; Score 19; DB 1; Length 2271;
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;
 Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 agctggcgctcccgcggtatcggaagccac 35
 Db 1896 AGCTGGCGCTCCCGGAGTCCCGAGCCAGCCAC 1862
 RESULT 13
 Q45334/c
 ID Q45334 standard; cDNA; 2271 BP.
 AC Q45334;
 DT 10-SEP-1994 (first entry)
 DE Human TLE-2 gene.
 KW TLE-2; transducin-like enhancer of split protein; cell fate;
 KW differentiation; cervix cancer; breast cancer; psoriasis; baldness;
 KW ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT cds 26..2257
 FT /tag= a
 FT W09407522-A.
 PN 14-APR-1994.
 PD 30-SEP-1993; U09339.
 PE 30-SEP-1992; US-954813.
 PR (UYIA) UNIV YALE.
 PA Artavanis-tsakonas S, Stifani S;
 DR WPI: 94-135221/16.
 DR P-PSDB: R51110.
 PT Transducin-like enhancer or split proteins and nucleic acids -
 PT are for treatment of disorders of cell fate or differentiation
 PT e.g. cervical cancer, breast cancer, psoriasis, baldness etc.
 PS Disclosure; Page 91-94; 147pp; English.
 CC The nucleotide and deduced aa sequences of human transducin-like
 CC enhancer of split proteins TLE-1 (Q45333, R51109), TLE-2 (Q45334,
 CC R51110), TLE-3 (Q45335, R51111) and TLE-4 (Q45336, R52953) were
 CC determined. The aa sequences were compared with that of
 CC Drosophila E(spl) m9/10 (R52955). Comparison of the WD-40 domains
 CC of these proteins defined the consensus residues shown in R52954.
 CC The Ccn motifs of the proteins were compared with those of SV40 T
 CC antigen, human c-myc, human p53, human A-myb and dorsal protein with
 CC respect to nuclear localization site, and casein-kinase and cdc2-
 CC kinase phosphorylation sites (sequences R52956-70).
 SQ Sequence 2271 BP; 437 A; 751 C; 672 G; 411 T;
 Query Match 54.3%; Score 19; DB 1; Length 2271;
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;
 Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 agctggcgctcccgcggtatcggaagccac 35
 Db 1896 AGCTGGCGCTCCCGGAGTCCCGAGCCAGCCAC 1862

RESULT

ID T93610/C
T93610 standard; DNA; 3946 BP.
AC T93610;
DT 27-APR-1998 (first entry)
DE Mycobacterium tuberculosis genomic DNA fragment (I).
E Mycobacterium tuberculosis; infection; diagnosis;
KW Tuberculosis; mycobacteria; antibiotic; vaccine; ss.
KK antimycobacterial; tuberculousis.
OS Mycobacterium tuberculosis.
PS WO9741252-A2.
PPN 06-NOV-1997.
PD PD
PF 18-APR-1997; E01973.
PE 29-APR-1996; DE-017184.
PR (GBFB) GBF GES BIOTECH FORSCHUNG GMBH.
PPA Espitia C, Honisch C, Moreno C, Singh M;
PPI WPI; 97-549750/50.
DR P-PSTB; W31852-55.
D New DNA and related proteins or RNA derived from M. tuberculosis - used for diagnosis of mycobacterial infections, monitoring vaccination and development of anti-mycobacterial agents Claim 1; Fig 9; 55pp; English.

PPT New claimed DNA (A) has one of 3 isolated Mycobacterium tuberculosis DNA sequences of 3946 bp (I) (T93610), 2653 bp (VI) (see T93611) or 440 bp (IX) (see T93612), or hybridises to, or is a fragment of these sequences. Also claimed are RNA transcripts of (A), and proteins encoded by (A). To isolate (I), a cosmid library of M. tuberculosis DNA was screened with degenerate probes (see T93621) containing GC-rich regions and designed to encode part of a proline-rich protein. (I) contains open reading frames (ORFs) for 4 proteins (see W31852-55). These ORFs can be amplified and cloned into vectors for expression in E. coli or other hosts. Clones (VI) and (IX) were obtained from a phage library and together encode 3 proteins (see W31851 and W31856-57). The claimed DNA sequences can be used for diagnosing tuberculosis and other mycobacterial infections in humans or animals, for identifying mycobacteria in (clinical) samples by hybridisation or amplification, including differentiation between strains, as well as for epidemiological studies, for monitoring vaccination or for the development of anti-mycobacterial drugs and vaccines.

SQ Sequence 3946 BP; 518 A; 1541 C; 1345 G; 542 T;

Query Match 53.7%; Score 18.8; DB 1; Length 3946;
Best Local Similarity. 76.7%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gap

DY 2 gctggcgccctcgcggtatcgaggac 31
 | ||||| | ||||||| ||||| |
DB 2826 gctggcgaccgcccccggctgatcgataac 2797

Search completed: September 28, 1999, 16:50:28
Job time: 7613 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 28, 1999, 16:41:07 : Search time 152.56 Seconds
(without alignments)
21.032 Million cell updates/sec

Title: US-09-037-657-30

Perfect score: 35

Sequence: 1 agctggcgccgctccggcgatcgaggccac 35

Scoring table: IDENTITY_NUC

Searched: 176461 seqs, 45838279 residues

Database : Issued Patents_NA.*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	19.2	54.9	6306	2	US-08-466-390-3
2	19.2	54.9	6306	2	US-08-470-950-3
3	19.2	54.9	6306	3	US-08-467-781-3
4	19.2	54.9	6306	3	US-08-195-487-3
5	19.2	54.9	6306	4	US-08-483-924-3
6	19.2	54.9	6306	5	PCT-US93-06160-3
7	18.6	53.1	1578	3	US-08-681-129-1
8	18.6	53.1	2543	3	US-08-555-669-11
9	18.4	52.6	1735	1	US-08-102-863-10
10	18.4	52.6	1735	1	PCT-US92-10885-10
11	18.2	52.0	30001	1	US-08-125-468-1
12	18.2	52.0	30001	4	US-08-474-933-1
13	17.8	50.9	4221	1	US-07-947-120-7
14	17.8	50.9	476	1	US-07-947-120-9
15	17.8	50.9	1820	1	US-08-173-508-7
16	17.8	50.9	4221	2	US-08-472-893A-7
17	17.8	50.9	476	2	US-08-472-893A-9
18	17.8	50.9	1325	3	US-08-306-691B-51
19	17.8	50.9	4244	4	US-08-460-694-1
20	17.8	50.9	1325	4	US-08-464-517-1
21	17.8	50.9	1317	4	US-08-464-517-34
22	17.8	50.9	44377	4	US-08-804-227C-7
23	17.8	50.9	573	4	US-08-290-665A-124
24	17.8	50.9	1325	5	PCT-US93-05000-1
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26	17.8	50.9	1317	5	PCT-US93-05000-36
27	17.8	50.9	1192	5	PCT-US93-06251-51
28	17.8	50.9	573	5	PCT-US95-10398-124
29	17.6	50.3	2614	4	US-08-795-868-15
30	17.6	50.3	685	5	PCT-US95-08137-1
31	17.6	50.3	685	5	PCT-US95-08137-3
32	17.4	49.7	1791	1	US-08-399-646-3
33	17.4	49.7	2056	1	US-08-399-646-13
34	17.4	49.7	1791	2	US-08-607-321-3
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36	17.4	49.7	11219	3	US-07-642-734C-1
37	17.4	49.7	1791	4	US-08-961-240-3

c 38 17.4 49.7 2056 4 US-08-961-240-13
c 39 17.4 49.7 1791 4 US-08-605-501-3
c 40 17.4 49.7 2056 4 US-08-605-501-13
c 41 17.4 49.7 1500 5 PCT-US93-08386-3
c 42 17.2 49.1 2750 2 US-08-136-277-1
c 43 17.2 49.1 1441 2 US-08-136-277-18
c 44 17.2 49.1 1748 2 US-08-255-471-8
c 45 17.2 49.1 2750 4 US-08-479-403-1

ALIGNMENTS

RESULT 1
US-08-466-390-3
: Sequence 3, Application US/08466390
: Patent No. 586562
: GENERAL INFORMATION:
: APPLICANT: TOKATLY, GARY
: APPLICANT: LIDGARD, GRAHAM P
: TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
: TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: TESTA, HURWITZ & THIBEAULT
: STREET: 125 HIGH STREET
: CITY: BOSTON
: STATE: MA
: COUNTRY: USA
: ZIP: 02110
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/466.390
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: PITCHER ESQ, EDMUND R
: REGISTRATION NUMBER: 27,829
: REFERENCE/DOCKET NUMBER: MTP-013
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 248-7000
: TELEFAX: (617) 248-7100
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6306 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..6306
: PUBLICATION INFORMATION:
: AUTHORS: COMPTON, DUANE A
: AUTHORS: SZILAK, ILYA
: AUTHORS: CLEVELAND, DON W
: TITLE: PRIMARY STRUCTURE OF NUMA, AN INTRANUCLEAR
: TITLE: PROTEIN THAT DEFINES A NOVEL PATHWAY FOR
: TITLE: SEGREGATION OF PROTEINS AT MITOSIS
: JOURNAL: J. Cell Biol.
: VOLUME: 116
: PAGES: 1395-1408
: DATE: 1992
US-08-466-390-3

Query Match 54.9%; Score 19.2; DB 2; Length 6306;
Best Local Similarity 87.5%; Pred. No. 44; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 3;

QY 6 ggcgcctcccgccgagtcgga 29
||| ||||| ||||| |||||
Db 3459 GCGGGCTCCCGGCTGAGCGGA 3482

RESULT 2

US-08-470-950-3
; Sequence 3, Application US/08470950
; Patent No. 5698439
; GENERAL INFORMATION:
; APPLICANT: TOURKATLY, GARY
; APPLICANT: LIDGARD, GRAHAM P
; TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
; TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,950
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESO, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: MTP-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6306 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..6306
; PUBLICATION INFORMATION:
; AUTHORS: COMPTON, DUANE A
; AUTHORS: SZILAK, ILYA
; AUTHORS: CLEVELAND, DON W
; TITLE: PRIMARY STRUCTURE OF NUMA, AN INTRANUCLEAR
; TITLE: PROTEIN THAT DEFINES A NOVEL PATHWAY FOR
; TITLE: SEGREGATION OF PROTEINS AT MITOSIS
; JOURNAL: J. Cell Biol.
; VOLUME: 116
; PAGES: 1395-1408
; DATE: 1992
US-08-470-950-3

Query Match 54.9%; Score 19.2; DB 2; Length 6306;
Best Local Similarity 87.5%; Pred. No. 44;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ggcgcctcccgccgagtcgga 29
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Db 3459 GCGGGCTCCCGGCTGAGCGGA 3482

RESULT 3

US-08-467-781-3
; Sequence 3, Application US/08467781
; Patent No. 5780596
; GENERAL INFORMATION:
; APPLICANT: TOURKATLY, GARY
; APPLICANT: LIDGARD, GRAHAM P
; TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
; TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,781
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESO, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: MTP-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6306 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..6306
; PUBLICATION INFORMATION:
; AUTHORS: COMPTON, DUANE A
; AUTHORS: SZILAK, ILYA
; AUTHORS: CLEVELAND, DON W
; TITLE: PRIMARY STRUCTURE OF NUMA, AN INTRANUCLEAR
; TITLE: PROTEIN THAT DEFINES A NOVEL PATHWAY FOR
; TITLE: SEGREGATION OF PROTEINS AT MITOSIS
; JOURNAL: J. Cell Biol.
; VOLUME: 116
; PAGES: 1395-1408
; DATE: 1992
US-08-467-781-3

Query Match 54.9%; Score 19.2; DB 3; Length 6306;
Best Local Similarity 87.5%; Pred. No. 44;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ggcgcctcccgccgagtcgga 29
||| ||||| ||||| |||||
Db 3459 GCGGGCTCCCGGCTGAGCGGA 3482

RESULT 4

US-08-195-487-3
; Sequence 3, Application US/08195487
; Patent No. 5783403
; GENERAL INFORMATION:
; APPLICANT: TOURKATLY, GARY
; APPLICANT: LIDGARD, GRAHAM P
; TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE

```

; TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,487
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/901,701
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: MTP-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6306 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..6306
; PUBLICATION INFORMATION:
; AUTHORS: COMPTON, DUANE A
; AUTHORS: SZILAK, ILLYA
; AUTHORS: CLEVELAND, DON W
; TITLE: PRIMARY STRUCTURE OF OF NUMA, AN INTRANUCLEAR
; TITLE: PROTEIN THAT DEFINES A NOVEL PATHWAY FOR
; TITLE: SEGREGATION OF PROTEINS AT MITOSIS
; JOURNAL: JOURNAL OF CELL BIOLOGY
; VOLUME: 116
; PAGES: 1395-1408
; DATE: MAR-1992
; US-08-195-487-3

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Query Match 54.9%; Score 19.2; DB 3; Length 6306;
Best Local Similarity 87.5%; Pred. No. 44;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 gcgcgcctccggcgatcgga 29
    ||| ||||| ||||| |||||
Db 3459 GCGGCGCTCCGGCGTGAGCGGA 3482

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RESULT 5
US-08-483-924-3
; Sequence 3, Application US/08483924
; Patent No. 5882876
; GENERAL INFORMATION:
; APPLICANT: TONKATLY, GARY
; APPLICANT: LIDGARD, GRAHAM P
; TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
; TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT

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; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,924
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: MTP-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6306 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..6306
; PUBLICATION INFORMATION:
; AUTHORS: COMPTON, DUANE A
; AUTHORS: SZILAK, ILLYA
; AUTHORS: CLEVELAND, DON W
; TITLE: PRIMARY STRUCTURE OF NUMA, AN INTRANUCLEAR
; TITLE: PROTEIN THAT DEFINES A NOVEL PATHWAY FOR
; TITLE: SEGREGATION OF PROTEINS AT MITOSIS
; JOURNAL: J. Cell Biol.
; VOLUME: 116
; PAGES: 1395-1408
; DATE: 1992
; US-08-483-924-3

Query Match 54.9%; Score 19.2; DB 4; Length 6306;
Best Local Similarity 87.5%; Pred. No. 44;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 gcgcgcctccggcgatcgga 29
    ||| ||||| ||||| |||||
Db 3459 GCGGCGCTCCGGCGTGAGCGGA 3482

RESULT 6
PCT-US93-06160-3
; Sequence 3, Application PC/TUS9306160
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
; TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US93/06160
FILING DATE: 19930621
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6306 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..6306
PUBLICATION INFORMATION:
AUTHORS: COMPTON, DUANE A
AUTHORS: SZILAK, ILLYA
AUTHORS: CLEVELAND, DON W
TITLE: PRIMARY STRUCTURE OF OF NUMA, AN INTRANUCLEAR
TITLE: PROTEIN THAT DEFINES A NOVEL PATHWAY FOR
TITLE: SEGREGATION OF PROTEINS AT MITOSIS
JOURNAL: JOURNAL OF CELL BIOLOGY
VOLUME: 116
PAGES: 1395-1408
DATE: MAR-1992
PCT-US93-06160-3

Query Match 54.9%; Score 19.2; DB 5; Length 6306;
Best Local Similarity 87.5%; Pred. No. 44;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 6 gcgcgcctccggcgatcgga 29
||| ||||| ||||| |||||
Db 3459 GCGGCGCTCCGCGGTGAGCGGA 3482

RESULT 7
US-08-681-129-1
Sequence 1, Application US/08681129
Patent No. 5738854
GENERAL INFORMATION:
APPLICANT: Mettenleiter, Thomas Cristoph
TITLE OF INVENTION: Pseudorabies virus vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Organon Teknika Corporation
STREET: 1330 Piccard Drive
CITY: Rockville
STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/681.129
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,446
FILING DATE: 02-JUN-1994
CLASSIFICATION: 424

APPLICATION NUMBER: EP 92.203.079.6
FILING DATE: 06-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1578 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Pseudorabies virus
STRAIN: Kaplan
US-08-681-129-1

Query Match 53.1%; Score 18.6; DB 3; Length 1578;
Best Local Similarity 72.7%; Pred. No. 81;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 1 agctggcgccctccggcgatcgga 33
||| ||||| ||||| |||||
Db 200 AGCTGGCGCCTCCGCGGTGAGCGGCC 232

RESULT 8
US-08-555-669-11
Sequence 11, Application US/08555669
Patent No. 5773248
GENERAL INFORMATION:
APPLICANT: Brewton, Richard G.
APPLICANT: Mayne, Richard
TITLE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,669
FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2543 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 47..2098
US-08-555-669-11

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,468
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Tsevdos, Estelle J
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,255-02
TELEPHONE: (201)831-3241
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 30001 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-125-468-1

Query Match 52.0%; Score 18.2; DB 1; Length 30001;
Best Local Similarity 74.2%; Pred. No. 77;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 agctggcgccctcccgggcgatcgaggc 31
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DB 26694 AGCTGGAGCGCTCTCGGCGACCGCGGTAGC 26664

RESULT 12

US-08-474-933-1/c
Sequence 1, Application US/08474933
Patent No. 5866410
GENERAL INFORMATION:
APPLICANT: Ryan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy
APPLICANT: Fantini, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: chlortetracycline and tetracycline formation and cosmids
TITLE OF INVENTION: useful therein
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: USA
ZIP: 07470
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,933
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,468
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Tsevdos, Estelle J
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,255-02
TELEPHONE: (201)831-3241
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 30001 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-474-933-1

Query Match 52.0%; Score 18.2; DB 4; Length 30001;
Best Local Similarity 74.2%; Pred. No. 77;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 agctggcgccctcccgggcgatcgaggc 31
||||| ||||| | |||||
DB 26694 AGCTGGAGCGCTCTCGGCGACCGCGGTAGC 26664

RESULT 13

US-07-947-120-7/c
Sequence 7, Application US/07947120
Patent No. 5538846
GENERAL INFORMATION:
APPLICANT: Meeker, Timothy C.
TITLE OF INVENTION: BCI-1 Locus Nucleic Acid Probes and
TITLE OF INVENTION: Assay Methods
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: Steuart Street Tower, 18th Fl., One Market
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/947,120
FILING DATE: 19920917
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 91-210-1
TELEPHONE: 415-777-9257
TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4221 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 142..1026
US-07-947-120-7

Query Match 50.9%; Score 17.8; DB 1; Length 4221;
Best Local Similarity 75.9%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 gctggcgccctcccgggcgatcgaggc 30
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DB 140 GCTGGGCTCTTCTCGGCGACGCTGGGAG 112

RESULT 14
US-07-947-120-9/c
; Sequence 9, Application US/07947120
; Patent No. 5338846
; GENERAL INFORMATION:
; APPLICANT: Meeker, Timothy C.
; TITLE OF INVENTION: Bcl-1 Locus Nucleic Acid Probes and
; TITLE OF INVENTION: Assay Methods
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: Steuart Street Tower, 18th Fl., One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/947,120
; FILING DATE: 19920917
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: 91-210-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-777-9257
; TELEFAX: 415-543-4219
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-07-947-120-9

Query Match 50.9%; Score 17.8; DB 1; Length 476;
Best Local Similarity 75.9%; Pred. No. 1.7e-02;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2 gctggcgccctccggcgccgagcgag 30
Db 471 GCTGGGGCTCTTCTGGGCGAGCTGGGAG 443

RESULT 15
US-08-173-508-7
; Sequence 7, Application US/08173508
; Patent No. 5616485
; GENERAL INFORMATION:
; APPLICANT: Bartfeld, Daniel
; APPLICANT: Butler, Michael J.
; APPLICANT: Hadary, Dany
; APPLICANT: Jenish, David
; APPLICANT: Krieger, Timothy
; TITLE OF INVENTION: STREPTOMYCES PROTEASES AND IMPROVED
; TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA

ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,508
; FILING DATE: 23-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 18740/125/CACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 672 5300
; TELEFAX: 202 672 5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1820 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 104..1720
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 104..244
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 245..1720
US-08-173-508-7

Query Match 50.9%; Score 17.8; DB 1; Length 1820;
Best Local Similarity 75.9%; Pred. No. 1.4e-02;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 7 cgcgcctccggcgccgagcgagccac 35
Db 1748 CACGCTCCGGGCGGGTTCGGAGCACCC 1776

Search completed: September 28, 1999, 16:41:09
Job time: 7055 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 28, 1999, 15:38:38 ; Search time 2095.87 seconds
(without alignments)
32.940 Million cell updates/sec

Title: US-09-037-657-30

Perfect score: 35
Sequence: 1 agctggcgccctcccgggcgagatcgaggagccac 35

Scoring table: IDENTITY_NUC

Searched: 2546578 seqs, 986266752 residues

Database :

EST:

- 1: em_est1:*
- 2: em_est2:*
- 3: em_est3:*
- 4: em_est4:*
- 5: em_est5:*
- 6: em_est6:*
- 7: em_est7:*
- 8: em_est8:*
- 9: em_est9:*
- 10: em_est10:*
- 11: em_est11:*
- 12: em_est12:*
- 13: em_est13:*
- 14: em_est14:*
- 15: em_est15:*
- 16: em_est16:*
- 17: em_est17:*
- 18: em_est18:*
- 19: em_est19:*
- 20: gb_est1:*
- 21: gb_est2:*
- 22: gb_est3:*
- 23: gb_est4:*
- 24: gb_est5:*
- 25: gb_est6:*
- 26: gb_est7:*
- 27: gb_est8:*
- 28: gb_est9:*
- 29: gb_est10:*
- 30: gb_est11:*
- 31: gb_est12:*
- 32: gb_est13:*
- 33: gb_est14:*
- 34: gb_est15:*
- 35: gb_est16:*
- 36: gb_est17:*
- 37: gb_est18:*
- 38: gb_est19:*
- 39: gb_est20:*
- 40: gb_est21:*
- 41: gb_est22:*
- 42: gb_est23:*
- 43: gb_est24:*
- 44: gb_est25:*
- 45: gb_est26:*
- 46: gb_est27:*
- 47: gb_est28:*
- 48: gb_est29:*
- 49: gb_est30:*
- 50: gb_est31:*
- 51: gb_est32:*
- 52: em_est20:*
- 53: em_est21:*

- 54: em_est22:*
- 55: em_est23:*
- 56: em_est24:*
- 57: em_est25:*
- 58: em_est26:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB	ID	Description
C 1	22.2	63.4	404	26	W63911 md90e12.r1
C 2	22.2	63.4	834	26	W82073 me96f06.r1
C 3	22.2	63.4	256	27	AA052662 mf41c04.r
C 4	22.2	63.4	341	28	AA105248 mp45h11.r
C 5	22.2	63.4	441	28	AA116255 mp06e12.r
C 6	22.2	63.4	525	29	AA124665 mp79e08.r
C 7	22.2	63.4	423	34	AA518890 v102h06.r
C 8	22.2	63.4	346	37	AA691737 vs13f12.r
C 9	21.2	60.6	473	39	AA885331 al60g08.s
10	21	60.0	435	26	W74180 zd75e07.s1
11	21	60.0	447	43	AI191353 qe32c09.s
12	20.2	57.7	319	48	AI574687 UI-R-GO-U
13	20.2	57.7	332	48	AI579568 UI-R-GO-U
14	19.8	56.6	335	36	C74272 C74272 Rice
15	19.8	56.6	209	41	AI016400 cv59h10.s
16	19.6	56.0	390	21	T84586 yd50d04.r1
C 17	19.6	56.0	407	26	W30648 mc14d08.r1
C 18	19.6	56.0	401	39	AA889310 ak27a06.s
C 19	19.6	56.0	328	43	AI197884 q148g01.x
C 20	19.6	56.0	251	45	AI356203 qy54g07.x
C 21	19.6	56.0	458	45	AI365982 ao9dcl1.x
C 22	19.6	56.0	223	45	AI393355 t909c07.x
C 23	19.6	56.0	361	46	AI401119 t926b06.x
C 24	19.6	56.0	355	47	AI470829 t189f02.x
C 25	19.6	56.0	241	49	AI640129 wa29e01.x
C 26	19.6	56.0	215	49	AI640362 wa17d02.x
C 27	19.4	55.4	465	26	W46604 zc32h10.s1
C 28	19.4	55.4	412	35	AA595903 nm65g03.s
C 29	19.4	55.4	445	36	AA622824 np35f03.s
C 30	19.2	54.9	219	28	AA091921 mm1518.se
C 31	19.2	54.9	407	39	AA880407 vx40d01.r
C 32	19.2	54.9	235	48	AI575060 UI-R-GO-U
C 33	19	54.3	308	20	T31953 EST41425.Hu
C 34	19	54.3	405	26	W57897 zd17d12.s1
C 35	19	54.3	447	27	AA042972 zk56d06.r
C 36	19	54.3	531	30	AA201099 LD03671.5
C 37	19	54.3	392	31	AA275781 vc26d10.r
C 38	19	54.3	176	32	AA336861 EST41510
C 39	19	54.3	566	33	AA391856 LD10795.5
C 40	19	54.3	500	33	AA392321 LD11158.5
C 41	19	54.3	465	35	AA557401 nl81h11.s
C 42	19	54.3	289	35	C26311 C26311 Rice
C 43	19	54.3	477	36	AA635631 nr35g12.s
C 44	19	54.3	570	37	AA695430 GM02819.5
C 45	19	54.3	521	37	AA695938 GM04804.5

ALIGNMENTS

RESULT 1
W63911/c

LOCUS md90e12.r1 Soares mouse embryo NbME13.5 404 bp mRNA

DEFINITION clone IMAGE:385294 5', mRNA sequence. EST 10-JUN-1996

ACCESSION W63911

NID 91371469

VERSION W63911.1 GI:1371469

On May 8, 1995 this sequence version replaced g1:800265.

Email: mousestewatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (Info@image.llnl.gov) for further information.
MGI:346877
Seq primer: -28m13 rev2 ET from Amersham

source

[illegible]

QY	1	agctggcgcgctccggcgcgatcggggagccac	35
	1		
	143	ATCAGGGGACCTCTGGTGGTTCAGGAGCCAC	109
Db			

Matches	27;	Conservative	0;	Mismatches	8;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

RESULT	5	
AA116255/c		
LOCUS	AA116255	441 bp. mRNA

AA105248/C	AA105248	341 bp	EST	13-FEB-1997
LOCUS	mp45h11.r1	Barstead	MPLEB1	Mus musculus
DEFINITION	mp45h11	Barstead	CDNA clone	IMAGE:572229 5'

[illegible]

NID
g1655001
1102010
1102010

SOURCE house mouse.

ORGANISM	Mus musculus
Pathogen	
Host	
Vector	
Reservoir	
Transmission	
Prevalence	
Incidence	
Significance	
Notes	

REFERENCE
1 (bases 1 to 341)

TITLE
JOURNAL
COMMENT

The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1293995.

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:352614

Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 435.

FEATURES
source

1. .441
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:577966"
/clone_lib="Soares 2NBMt"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGTGGGAGCGCGGTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT
ORIGIN

94 a 139 c 116 g 92 t

Query Match

Best Local Similarity 63.4%; Score 22.2; DB 28; Length 441;

Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 agctgcgcgcctcccgccgagatcgaggccac 35

Db 237 ATCAGGGGAGCCCTCGGTGGTTTCAGGAGCCAC 203

RESULT 6

AA124665/c

LOCUS

DEFINITION

mp79608.r1 Soares 2NBMt Mus musculus cDNA clone IMAGE:575462 5',
similar to TR:G203113 G203113 BETA'-CHAIN CLATHRIN ASSOCIATED
PROTEIN COMPLEX AP-1. ; mRNA sequence.

ACCESSION

NID

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

The WashU-HHMI Mouse EST Project

Unpublished (1996)

On Sep 12, 1996 this sequence version replaced gi:1290543.

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:350110

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 449.

FEATURES

source

1. .525
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:575462"
/clone_lib="Soares 2NBMt"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGTGGGAGCGCGGTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT

106 a 168 c 136 g 115 t

ORIGIN

Query Match

Best Local Similarity 63.4%; Score 22.2; DB 29; Length 525;

Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 agctgcgcgcctcccgccgagatcgaggccac 35

Db 236 ATCAGGGGAGCCCTCGGTGGTTTCAGGAGCCAC 202

RESULT 7

AA518890/c

LOCUS

DEFINITION

AA518890 423 bp mRNA EST 16-JUL-1997
v102h06.r1 Barstene mouse myotubes MPLRB5 Mus musculus cDNA clone
IMAGE:902651 5' similar to TR:G203113 G203113 BETA'-CHAIN CLATHRIN
ASSOCIATED PROTEIN COMPLEX AP-1. ; mRNA sequence.

ACCESSION

NID

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

The WashU-HHMI Mouse EST Project

Unpublished (1996)

On Sep 12, 1996 this sequence version replaced gi:1397524.

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouse@watson.wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:523315

FEATURES

```

seq primer: 20m13 rev2 Errfrom Amersham.
Location/Qualifiers
1. .423
/organism="Mus musculus"
/strain="C3H"
/db_xref="taxon:10090"
/clone_image=902651"
/clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand CDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTAGCAATCGAATGGAGGCGGCCCTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[AATCGGACCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT73 vector.
Library constructed by Bob Barstead. The C2C12 cell line
(available from ATCC, catalog # CRL-1772) differentiates
rapidly, forming contractile myotubes and producing
characteristic muscle proteins."
92 a 127 c 114 g 89 t 1 others

BASE COUNT
ORIGIN

Query Match 63.4%; Score 22.2; DB 34; Length 423;
Best Local Similarity 77.1%; Pred. No 75;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 agctggcgcgctcccgcgcgatcgaggagccac 35
| | | | | | | | | | | | | | | | | | | |
DB 275 ATCAGGAGGACCTCTCGGTGGTGTTCAGGAGCCAC 241

```

RESULT 8
AA691737/C

8
RESULT
AA691737/c
LOCUS
vsl3f12.r1 Barstead mouse EST 16-DEC-1997
DEFINITION clone IMAGE:1138127 5' similar to SW:ADBI_RAT P52303 BETA-ADAPTIN 1
; , mRNA sequence.
AA691737
AA691737.1 GI:2692675
g2692675
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 346)
AUTHORS
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennan,G., Soares,B., Willson,R. and
Waterston,R.
TITLE
The WashU-HHMI Mouse EST Project
JOURNAL
Unpublished (1996)
COMMENT
On Sep 12, 1996 this sequence version replaced gi:1393359.

Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School
of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 222.

FEATURES

```

"align" quality sequence stop: 222;
Location/Qualifiers
1. 346
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/map="Xq28"
/clone="IMAGE:1138127"
/clone_lib="Barstead mou
/dev stage="8 weeks"

```

polylinker; Site_1: EcoR
from 8 week old mouse
irradiation with 1400 Gy
with a Not I - oligo(dT)
[5'-TCTTCAGACTCTGAATGGGA
T 3']; double-stranded
adaptors (Not ICGGATCCCTTG
into the Not I and Eco R
vector. Library construc
74 a 106 c 88 g 71

BASE COUNT
ORIGIN

vector: library constructed
74 a 106. c 88 g 78 t

Query Match

```
Query Match      63.4%; Score 22.2; DB 37; Length 346;
Best Local Similarity 77.1%; Pred. No. 73;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

Qy. 13.

Qy 1 agctggcgcgccctcccgggcgatcgggagccac 35
| | | | | | | | | | | | | | | | | | | | | |
Db 234 ATCAGGGGAGCCTCCTGGGTGGTTCAGGAGCCAC 200

RESULT 9
AA885331

RESULT	9
AA885331	
LOCUS	AA885331 473 bp mRNA EST
DEFINITION	al60908.s1 Soares_NFL_T_GSC_s1 Homo sapiens cDNA clone IMAGE:1461758 3' similar to contains Alu repetitive element., mRNA

ACCESSION

sequence.
AA885331
92994408
AA885331.1. GI:2994408
EST.
human.
Homo sapiens.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 473)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1798638.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LNL ; contact
IMAGE Consortium (info@image.llnl.gov) for further informa
Insert Length: 597 Std Error: 0.00
Seq Primer: -40ml3 fwd. ET from Amer\$ham
High quality sequence stop: 470.

FEATURES

```

"seq_quality sequence stop": 470,
  "Location/Qualifiers":
    1. .473
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /map="21"
      /clone="IMAGE:1461758"

```

```

/clone_lib="Soares_NFL_T_GBC_S1"
/notes="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CGAP-GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT      94 a 144 c 139 g 96 t
ORIGIN

Query Match      60.6%; Score 21.2; DB 39; Length 473;
Best Local Similarity 76.5%; Pred. No. 1.6e+02;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY  2  gctggcgccctcccgccgagtcggagccac 35
|||||  |||||||  |||||||  |||||||  ||
Db  364  GCTGGCGCCCTCCCGTCCCATGGGAGAGAC 397

RESULT 10
LOCUS      W74180      435 bp      mRNA      EST      17-OCT-1996
DEFINITION      zdfse07.s1 Soares_fetal_heart_NBHL19W Homo sapiens cDNA clone
IMAGE:346500 3', mRNA sequence.
ACCESSION      W74180
NID      g1384624
VERSION      W74180.1 GI:1384624
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 435)
AUTHORS      Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Ruhlberg,T., Soares,M., Tan,F.,
Treviskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.
TITLE      The WashU-Merck EST Project
JOURNAL      Unpublished (1995)
COMMENT      On Nov 29, 1993 this sequence version replaced gi:430390.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 575 Std Error: 0.00
Seq primer: mob.REGA-ET
High quality sequence stop: 341.
Location/Qualifiers
1. .435
/organism="Homo sapiens"
/db_xref="GDB:1271875"
/db_xref="taxon:9606"
/clone_lib="Soares_fetal_heart_NBHL19W"
/clone="IMAGE:346500"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
(5'-TGTTACCAATCTGAAGTGGGAGCCGATCTTTTTTTTTTTT 3'),
ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library was constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHL19W."
BASE COUNT      98 a 140 c 136 g 83 t
ORIGIN

```

```

strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACCAATCTGAAGTGGGAGCCGATCTTTTTTTTTTTT 3'),
ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library was constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHL19W."
BASE COUNT      79 a 131 c 117 g 104 t 4 others
ORIGIN

Query Match      60.0%; Score 21; DB 26; Length 435;
Best Local Similarity 82.8%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2  gctggcgccctcccgccgagtcggag 30
|||||  |||||||  |||||||  |||||||  ||
Db  377  GCTGGCGCCCTCCCGTCCCATGGGAG 405

RESULT 11
LOCUS      AI191353      447 bp      mRNA      EST      29-OCT-1998
DEFINITION      qe32c09.s1 Soares_fetal_lung_NBHL19W Homo sapiens cDNA clone
IMAGE:1740688 3', mRNA sequence.
ACCESSION      AI191353
NID      93742562
VERSION      AI191353.1 GI:3742562
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 447)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      On May 8, 1995 this sequence version replaced gi:801250.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 715 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
1. .447
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1740688"
/clone_lib="Soares_fetal_lung_NBHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: lung; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
(5'-TGTTACCAATCTGAAGTGGGAGCCGATCTTTTTTTTTTTT 3'),
ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library was constructed by
Soares and M.Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NBHL19W."
BASE COUNT      88 a 140 c 136 g 83 t
ORIGIN

```

DTN

found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 349 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.

FEATURES
source
1..209
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1641667"
/sex="male"
/lab_host="DH108"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5',
TGTTACCATCTGAGTGGGCGCGCCCAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cots, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 31 a 73 c 77 g 28 t
ORIGIN

Query Match 56.6%; Score 19.8; DB 41; Length 209;
Best Local Similarity 77.4%; Pred. No. 4.2e+02;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 agctggcgccctccggcgatcgaggc 31
||||| ||||| ||||| ||||| |||||
Db 28 AGCGGGGCACCTGCGGGCGTCCGGAAGC 58

Search completed: September 28, 1999, 15:38:41
Job time: 3309 sec

C74272.1 GI:2442501
EST.
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Poaceae; Oryza.
1 (bases 1 to 335)
Sasaki, T. and Yamamoto, K.
Rice cDNA from panicle
Unpublished (1997)
On May 8, 1995 this sequence version replaced gi:801536.

Contact: Takuji Sasaki
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2-1-2 Kannondai, Tsukuba
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Japan 305
Tel: 0298-38-7441
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FEATURES
source
1..335
Location/Qualifiers
/organism="Oryza sativa"
/strain="Nipponbare"
/db_xref="taxon:4530"
/clone="E30775.4A"
/clone_lib="Rice panicle shorter than 3cm"
/dev_stage="shorter than 3cm"
/note="Organ: panicle"
56 a 105 c 100 g 60 t 14 others
ORIGIN

Query Match 56.6%; Score 19.8; DB 36; Length 335;
Best Local Similarity 75.0%; Pred. No. 4.5e+02;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 4 tggcgccctccggcgatcgaggccac 35
||||| ||||| ||||| ||||| |||||
Db 163 TGGCGCTCTTCNCCGTCGGATCGGAGTCCAC 194

RESULT 15
AI016400 209 bp mRNA EST 27-AUG-1998
LOCUS
DEFINITION
ov59h10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1641667
3' similar to contains MER22.t3 MER22 repetitive element ;, mRNA
sequence.
ACCESSION
NID AI016400
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 209)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Nov 29, 1993 this sequence version replaced gi:636002.

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Email: Robert.Strausberg@nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be